

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	AA967989	Human B lymphocyte
2	1149	100.0	288	AA967989	B7-1. Homo sapien
3	1149	100.0	288	AAW38414	Human B7 protein s
4	1149	100.0	288	AAW67804	Human B7-2 antigen
5	1149	100.0	288	AAW73640	Human B lymphocyte
6	1149	100.0	288	AAW337087	Human B lymphocyte
7	1149	100.0	288	AAV99966	Human B7 protein.
8	1149	100.0	288	AAV44289	Human B7.1 co-stim
9	1149	100.0	288	AAV54920	Human B7.1 protein
10	1149	100.0	288	AAU05121	Colorectal tumour
	1149	100.0	288	AAV19959	Human B lymphocyte

FT Misc-difference 207..209
 FT /label= see above
 FT Misc-difference 211..213
 FT /label= see above
 FT Misc-difference 226..228
 FT /label= see above
 FT Misc-difference 232..234
 FT /label= see above
 FT 35..138
 FT /label= Ig V-set domain
 FT 139..236
 FT /label= Ig C-set domain
 FT XX

PN WO9503408-A.

XX 02-FEB-1995.

PD 26-JUL-1994; 94WO-US08423.

XX 26-JUL-1993; 93US-0101624.

PR 19-AUG-1993; 93US-0109393.

PR 03-NOV-1993; 93US-0147773.

XX (DAND) DANA FARBER CANCER INST INC.

PA (REPK) REPLIGEN CORP.

XX Freeman GJ, Gray GS, Greenfield E, Nadler LM;

PI WPI; 1995-075236/10.

DR N-PSDB; AAQ81371.

XX Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful

XX for enhancing or suppressing T-cell mediated immune responses

XX Disclosure; pages 111-113; 175pp; English.

XX Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,

XX cell line Raji, clone no. 13. Its position in the genome is

XX chromosome/segment 3. It was published by Freeman, F.J. et al.,

XX J. of Immunology, 143: 8: 2714-2722, 15th October 1989. It can be

XX found in Genbank at Accession no. M27533. The encoded protein,

XX R67989, binds both human CTLA4 and human CD28. It is related

XX to human hb7-2 (see Q81351) and murine hb7 (see Q81372).

XX Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 16; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.2e-103;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIVYQKQKMLVLTMSGDMNIWPE 60

DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIVYQKQKMLVLTMSGDMNIWPE 86

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTS 120

DB 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTS 146

QY 121 ISDFEPTSNIRRIICSTSGGFPPEHLVLENGEELNAINTTVSQDPETELYAVSSKLDF 180

DB 147 ISDFEPTSNIRRIICSTSGGFPPEHLVLENGEELNAINTTVSQDPETELYAVSSKLDF 206

QY 181 NMTTNHSMCLIKYGLHVRVNTQFNWNTTKQEHFPDN 216

DB 207 NMTTNHSMCLIKYGLHVRVNTQFNWNTTKQEHFPDN 242

RESULT 2

AAW38414

ID AAW38414 standard; Protein; 288 AA.

XX XX

XX AAW38414

XX AAW38414 standard; Protein; 288 AA.

XX XX

XX AAW38414

XX XX

XX AAW38414

XX XX

XX AAW38414

XX XX

XX AAW38414

XX XX

XX AAW38414

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XX AAW38414

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XX AAW38414

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XX AAW38414

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XX XX

XX AAW38414

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XX AAW38414

XX XX

XX AAW38414

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XX AAW38414

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XX AAW38414

XX XX

XX AAW38414

XX XX

XX AAW38414

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XX AAW38414

XX XX

XX AAW38414

XX XX

XX AAW38414

DT 08-APR-1998 (first entry)

XX B7-1.

DE Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

XX Screening; inhibitor; enhancer; binding; CD28; B7-1.

QY 121 ISDFEIPSNIRRIICSTSGGFPPEHLISWLENGEELNAINITVSDPETELAVSSKLDLF 180
 Db 147 ISDFEIPSNIRRIICSTSGGFPPEHLISWLENGEELNAINITVSDPETELAVSSKLDLF 206
 QY 181 NMTNHSFMCILIKYGHRLRVNOTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGHRLRVNOTFNWNTTKQEHFPDN 242

RESULT 5

AAB37087
 ID AAB37087 standard; Protein; 288 AA.

XX
 AC AAB37087;

XX
 DT 28-MAR-2001 (first entry)

XX
 DE Human B lymphocyte antigen B7-1.

XX
 KW Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
 KW antigen; extracellular domain; CTLA4; immunoglobulin constant region;
 KW immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;
 KW T cell-mediated immune response; transplantation; vaccination.

XX
 OS Homo sapiens.

XX
 PN US130316-A.

XX
 PD 10-OCT-2000.

XX
 PF 26-JUL-1994; 94US-0280757.

XX
 PR 26-JUL-1993; 93US-0101624.

XX
 PR 19-AUG-1993; 93US-0109393.

XX
 PR 03-NOV-1993; 93US-0147773.

XX
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (REPK) REPLIGEN CORP.

XX
 PI Freeman GJ, Nadler LM, Gray GS, Greenfield E;

XX
 DR WPI; 2000-655681/63.

XX
 DR N-PSDB; AAC84051.

XX
 PT Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for
 PT enhancing or suppressing T cell-mediated immune responses, especially
 PT during tissue, skin or organ transplantation, or in graft-versus-host
 PT disease

XX
 PS Disclosure; Column 87-90; 83pp; English.

XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC fusion protein comprising a first nucleotide sequence encoding a first
 CC peptide, and a second nucleotide sequence encoding a second peptide.
 CC The first nucleotide sequence hybridizes in 6 X sodium chloride/sodium
 CC citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C
 CC to a portion of a nucleotide sequence which encodes a human or murine
 CC B lymphocyte antigen (B7-2) extracellular domain. The first peptide has
 CC the ability to bind CD28 or CTLA4. The first peptide has an amino acid
 CC sequence that is identical or at least 50% identical with the
 CC extracellular domain of a human B7-2 peptide (AAB37085). The second
 CC peptide is especially an immunoglobulin constant region. This sequence
 CC represents the human B lymphocyte antigen B7-1. The sequence is used for
 CC comparison with the B7-2 sequence. The human B7-2 protein is an example
 CC of a first peptide sequence of the invention. The nucleic acid molecules
 CC are useful in various expression vectors to direct synthesis of the
 CC corresponding proteins or peptides in a variety of hosts, particularly
 CC eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic
 CC acids are also useful for enhancing the immunogenicity of a mammalian
 CC cell, e.g. tumour cell (sarcoma) or an antigen presenting cell
 CC (macrophage). The fusion proteins or peptides are useful for enhancing or
 CC suppressing T cell-mediated immune responses, e.g. in situations of
 CC tissue, skin or organ transplantation, or in graft-versus-host disease.

CC The proteins are also useful for enhancing the efficacy of vaccination
 CC against a variety of pathogens, and may also be used to upregulate an
 CC immune response against a particular pathogen during an infection or
 CC against a tumour in a tumour-bearing host.

XX
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;

Best Local Similarity 100.0%; Pred. NO. 3.2e-103;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVTHVTKEVATLSGCHNVSVBELAQTRIVYQKEKKVLTMMSGDMNIWPE 60
 Db 27 GLSHFCGVTHVTKEVATLSGCHNVSVBELAQTRIVYQKEKKVLTMMSGDMNIWPE 86

QY 61 YKNTIFDITNNLSIVILALRPDSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTS 120
 Db 87 YKNTIFDITNNLSIVILALRPDSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTS 146

QY 121 ISDFEIPSNIRRIICSTSGGFPPEHLISWLENGEELNAINITVSDPETELAVSSKLDLF 180
 Db 147 ISDFEIPSNIRRIICSTSGGFPPEHLISWLENGEELNAINITVSDPETELAVSSKLDLF 206

QY 181 NMTNHSFMCILIKYGHRLRVNOTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGHRLRVNOTFNWNTTKQEHFPDN 242

RESULT 6

AAY99966
 ID AAY99966 standard; Protein; 288 AA.

XX
 AC AAY99966;

XX
 DT 10-JAN-2001 (first entry)

XX
 DE Human B7 protein.

XX
 KW B7; human; B cell activation antigen; B lymphocytes;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW herpes simplex; influenza; common cold; HIV.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers

XX
 FH Peptide 1..34

XX
 FT /label= signal_peptide

XX
 FT Domain 35..242

XX
 FT /label= Extracellular_domain

XX
 FT Domain 35..138

XX
 FT /label= "Ig V-set domain"

XX
 FT Modified-site 53..55

XX
 FT /note= "N-linked glycosylation site"

XX
 FT Modified-site 89..91

XX
 FT /note= "N-linked glycosylation site"

XX
 FT Modified-site 98..100

XX
 FT /note= "N-linked glycosylation site"

XX
 FT Domain 139..236

XX
 FT /label= "Ig C-set domain"

XX
 FT Modified-site 186..188

XX
 FT /note= "N-linked glycosylation site"

XX
 FT Modified-site 207..209

XX
 FT /note= "N-linked glycosylation site"

XX
 FT Modified-site 211..213

XX
 FT /note= "N-linked glycosylation site"

XX
 FT Modified-site 226..228

XX
 FT /note= "N-linked glycosylation site"

XX
 FT Modified-site 232..234

XX
 FT /note= "N-linked glycosylation site"

XX
 FT Domain 243..269

XX
 FT /label= Transmembrane_domain

XX
 FT Domain 270..288

XX
 FT /label= Intracellular_domain

XX US6071716-A.
 XX 06-JUN-2000.
 XX 15-NOV-1993; 930S-0153262.
 XX 28-AUG-1991; 910S-0751306.
 XX 01-OCT-1990; 900S-0591300.
 XX (DAND) DANA FARBER CANCER INST INC.
 XX Nadler LM, Freeman GJ, Freedman AS;
 XX WPI: 2000-422081/36.
 XX N-PSDB; AA61328.
 XX New polynucleotides encoding a B7 activation antigen, useful for
 PT regulating T cell mediated immune responses or viral diseases -
 XX
 XX Claim 1; Fig 4; 36pp; English.
 XX The present sequence is the unique human B cell activation antigen B7
 CC protein. The cDNA encoding this sequence was isolated from a Burkitt
 CC lymphoma cell line cDNA library. Selection of cDNA clones was based
 CC on expression of B7, as detected by the anti-B7 monoclonal antibody.
 CC The human B7 cDNA was used in hybridisation analysis to isolate the
 CC murine B7 cDNA (see AAA61329). The B7 nucleic acid sequences may be
 CC used to generate transgenic, knock-out animals which, in turn, are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The expressed B7 protein is useful for enhancing or
 CC blocking activated T cell mediated immune responses and immune
 CC function. Modification of B7 expression is useful in the treatment of
 CC autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis),
 CC herpes simplex, influenza, the common cold and HIV. It is also useful
 CC in tissue and organ transplantation.
 XX
 XX Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVLELAQRIYQKEKKMVLTMMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVLELAQRIYQKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTS 120
 Db 87 YKNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSDPETELAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSDPETELAVSSKLD 206
 QY 181 NMTNHSFCLIKYGLHRYNQTFNNTTQEHFPDN 216
 Db 207 NMTNHSFCLIKYGLHRYNQTFNNTTQEHFPDN 242
 RESULT 7
 AAY44289
 ID AAY44289 standard; Protein; 288 AA.
 XX AAY44289;
 XX 29-FEB-2000 (first entry)
 XX Human B7.1 co-stimulatory molecule.
 XX Human B7.1 co-stimulatory molecule; antigen presenting cell;
 KW immune response; cell surface receptor; Major histocompatibility complex;
 KW MHC classII; proton motor force; mitochondrial membrane potential;

KW mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;
 KW neurodegenerative disorder.
 XX Homo sapiens.
 XX WO9953953-A2.
 XX 28-OCT-1999.
 XX 30-MAR-1999; 99WO-US06874.
 XX 17-APR-1998; 98US-0082250.
 XX 29-JUL-1998; 98US-0094519.
 XX 24-SEP-1998; 98US-0101580.
 XX (UYVE-) UNIV VERMONT.
 XX Newell MK;
 XX WPI: 2000-096773/08.
 XX N-PSDB; AA29320.
 XX Use of cell surface and membrane characteristics for developing
 PT products for treating cancers, autoimmune diseases or neurodegenerative
 PT diseases -
 XX
 XX Disclosure; Page 115; 123pp; English.
 XX The present sequence is human B7.1 co-stimulatory molecule. This is
 CC a glycoprotein on the surface of antigen presenting cells. This is
 CC involved in stimulation of an immune response by its ability to interact
 CC with various immune cell surface receptors. The regulation of cell
 CC surface expression of MHC classII and co-stimulatory molecule B7 can be
 CC manipulated by regulating the intracellular dissipation of proton motor
 CC force which can be assessed in terms of mitochondrial membrane potential.
 CC These methods can be used for regulating cell growth and division to
 CC control disease processes by manipulating mitochondrial metabolism and
 CC the expression of cell surface immune proteins. They can be used for
 CC treating diseases associated with excessive cellular division, aberrant
 CC differentiation, and premature cellular death, e.g. cancers, autoimmune
 CC diseases, neurodegenerative disorders etc.
 XX
 XX Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVLELAQRIYQKEKKMVLTMMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVLELAQRIYQKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTS 120
 Db 87 YKNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSDPETELAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINITVSDPETELAVSSKLD 206
 QY 181 NMTNHSFCLIKYGLHRYNQTFNNTTQEHFPDN 216
 Db 207 NMTNHSFCLIKYGLHRYNQTFNNTTQEHFPDN 242
 RESULT 8
 AAY54920
 ID AAY54920 standard; Protein; 288 AA.
 XX AAY54920;
 XX 14-FEB-2000 (first entry)
 XX

DE Human B7.1 protein sequence.

KW Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;

KW IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.

XX

OS Homo sapiens.

XX

PN US5994104-A.

XX

PD 30-NOV-1999.

XX

PF 08-NOV-1996; 96US-0751767.

XX

PR 08-NOV-1996; 96US-0751767.

XX

PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

XX

PI Anderson RJ, Prentice HG, MacDonald ID;

XX

DR WPI; 2000-038261/03.

DR N-PSDB; AAZ40022.

XX

PT Nucleic acid constructs encoding interleukin-12 fusion proteins useful

PT for treating leukemia and other cancers -

XX

PS Example; Fig 10; 73pp; English.

XX

CC This sequence represents the human B7.1 protein sequence.

CC The invention relates to an isolated nucleic acid construct (I)

CC comprising a region encoding an interleukin-12 (IL-12) fusion protein

CC (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker

CC peptide (joining the subunits)) and a region encoding a B7 protein. (I)

CC may be used to produce IL-12 fusion proteins according to standard

CC recombinant DNA methodologies. The fusion proteins may be produced either

CC in vitro in a fermentation culture or in vivo as part of a gene therapy

CC protocol (in this case (I) is used to transform a patients cells, which

CC then secrete the functional polypeptide to supplement the patients own

CC production of IL-12 or to rectify mutations which lead to the expression

CC of inactive polypeptides). The fusion proteins produced in this way may

CC be used to treat any disease which responds to IL-12 such as tumours

CC (both solid and dispersed of the kidney, breast, colon, ovarian and

CC cervical tumours and melanomas) and in particular, tumours of the blood

CC such as leukaemia. Alternatively, the polypeptides may be used as

CC antigens in the production of antibodies to IL-12 and to assay for

CC agonists and antagonists of its activity. The antibodies and antagonists

CC may be used to inhibit the activity of IL-12. (I) may also be used

CC diagnostically as a probe which hybridizes to sequences encoding IL-12

CC and the antibodies may be used to detect the presence of IL-12

CC polypeptides in samples. They may be used diagnostically to quantitate

CC the expression of the polypeptide by patients and hence which subjects

CC may be in need of restorative therapy.

XX

SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.2e-103;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKVATILSCGHNVSEELAQTRIYQKEKKMVLTMMSGDMNIWPE 60

DB 27 GLSHFCSGVIHVTKEVKVATILSCGHNVSEELAQTRIYQKEKKMVLTMMSGDMNIWPE 86

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 120

DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 146

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINNTVTSQDPETELYAVSSKLDIF 180

DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINNTVTSQDPETELYAVSSKLDIF 206

QY 181 NMTTNHSPCLIKYGHRLRYNQTFNNWTTKOEHPDN 216

DB 207 NMTTNHSPCLIKYGHRLRYNQTFNNWTTKOEHPDN 242

RESULT 9

AAU05121

ID AAU05121 standard; Protein; 288 AA.

XX

AC AAU05121;

XX

DT 24-OCT-2001 (first entry)

XX

DE Colorectal tumour antigen CD80.

XX

KW Colorectal cancer; immunostimulant; cytostatic; immune response;

KW adenocarcinoma; allogeneic tumour cell; SW620 cell; COLO 205 cell;

KW SW403 cell; colon; breast; lung; prostate; cancer; vaccine;

KW tumour antigen CD80.

XX

OS Homo sapiens.

XX

PN WC200154716-A2.

XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-US02731.

PR 27-JAN-2000; 2000US-0178498.

PR 28-FEB-2000; 2000US-0185335.

XX

PA (KIMM-) KIMMEL CANCER CENT SIDNEY.

PA (IMMU-) IMMUNE RESPONSE CORP.

PI Sobol RE, Shawler DL, Bartholomew RM, Carlo DJ, Gold DP;

XX

DR WPI; 2001-502616/55.

DR N-PSDB; AAS11426.

XX

PT New composition comprising an allogeneic tumour cell, useful for

PT stimulating an immune response in a patient having an adenocarcinoma,

PT especially useful for treating colorectal, breast, lung or prostate

PT cancer -

XX

PS Example 2; Page 130-131; 131pp; English.

XX

CC The invention relates to a composition for stimulating an immune response

CC in a patient having an adenocarcinoma or colorectal cancer. The

CC composition comprises an allogeneic tumour cell selected from SW620 cell,

CC COLO 205 cell and SW403 cell, and a physiological carrier. The allogeneic

CC cell stimulates an immune response to an autologous tumour cell in the

CC patient. The composition is useful for stimulating an immune response in

CC a patient having an adenocarcinoma, e.g. colon, breast, lung or prostate

CC adenocarcinoma. The use of allogeneic tumour cells provides a generic

CC source of antigen that can be administered to a variety of patients, in

CC contrast to using autologous tumour cells, which must be isolated from

CC each individual patient. The allogeneic cells are suitable as a cancer

CC vaccine and can stimulate an immune response against autologous tumour

CC cells of a cancer patient. The present sequence represents the amino acid

CC sequence of colorectal tumour antigen CD80 used in the method of the

CC invention.

XX

SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 22; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.2e-103;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKVATILSCGHNVSEELAQTRIYQKEKKMVLTMMSGDMNIWPE 60

DB 27 GLSHFCSGVIHVTKEVKVATILSCGHNVSEELAQTRIYQKEKKMVLTMMSGDMNIWPE 86

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 120

DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 146

QY 121 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
 QY 181 NMTNHSFMCCLIKYGLRVNQTNNWTTKQEHFPDN 216
 Db 207 NMTNHSFMCCLIKYGLRVNQTNNWTTKQEHFPDN 242

RESULT 10

AAE19959
 ID AAB19959 standard; Protein; 288 AA.
 XX
 AC AAB19959;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Human B lymphocyte antigen B7.
 XX
 KW Human; B7; B lymphocyte; antigen; T cell costimulatory molecule;
 KW CD28; CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;
 KW metastasis; antitumour; therapy.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..34
 FT /label= Signal_peptide
 FT Protein 35..288
 FT /label= Mature_protein
 FT Domain 35..242
 FT /note= "extracellular domain"
 FT Domain 243..269
 FT /note= "transmembrane domain"
 FT Domain 270..288
 FT /note= "intracellular domain"
 FT Domain 35..138
 FT /note= "immunoglobulin V-set domain"
 FT Domain 139..236
 FT /note= "immunoglobulin C-set domain"
 FT Modified-site 53..55
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 89..91
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 98..100
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 186..188
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 207..209
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 211..213
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 226..228
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 232..234
 FT /note= "Asn is N-glycosylated"

XX US6149905-A.

XX 21-NOV-2000.

XX 23-SEP-1998; 98US-0159135.

XX 03-NOV-1993; 93US-0147772.

XX (GENY) GENETICS INST INC.
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (HARD) HARVARD COLLEGE.

XX Baskar S, Glimcher LH, Freeman GJ, Ostrand-Rosenberg S;
 PI Nadler LM;

XX WPI; 2001-079388/09.

DR N-PSDB; AAA89224.

XX
 PT Modifying tumor cell for treating tumors, reducing metastatic spread,
 PT inhibiting recurrence of tumor and increasing immunogenicity, involves
 PT transfecting tumor cells with a nucleic acid encoding B7 molecule -

XX
 PS Claim 4; Column 31-34; 24pp; English.

XX
 CC The present sequence is that of human lymphocyte antigen B7, a T
 CC cell costimulatory molecule that binds to CD28 and CTLA4. Tumour
 CC cells modified to express a T cell costimulatory molecule,
 CC especially B7, are disclosed. The tumour cells are modified by
 CC transfection with a nucleic acid encoding the T cell costimulatory
 CC molecule, by using an agent which induces or increases expression
 CC of the T cell costimulatory molecule on the tumour cell surface, or
 CC by coupling the T cell costimulatory molecule to the tumour cell
 CC surface. Tumour cells further modified to express major
 CC histocompatibility complex (MHC) class I and/or class II molecules,
 CC or in which expression of an MHC associated protein, the invariant
 CC chain, is inhibited are also disclosed. The modified tumour cells
 CC are used to treat a patient with a tumour, preventing or inhibiting
 CC metastatic spread or tumour recurrence. The tumour may be a
 CC melanoma, a neuroblastoma, a leukaemia or a carcinoma. A method for
 CC specifically inducing a CD4+ T cell response against a tumour, and a
 CC method for treating a tumour by modification of tumour cells in vivo
 CC are also disclosed. The treatment methods increase the immunogenicity
 CC of the tumour cell in vivo. The antitumour T cell-mediated immune
 CC response is effective both against the modified tumour cells and the
 CC unmodified tumour cells from which the modified cells were derived.
 CC Thus, the effector phase of the antitumour response induced by the
 CC modified tumour cells is not dependent upon expression of a
 CC costimulatory molecule on the tumour cells.

XX Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 22; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKMYLTMMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKMYLTMMSGDMNIWPE 86

QY 61 YKNTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVSKADFTPS 120

Db 87 YKNTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVSKADFTPS 146

QY 121 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180

Db 147 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206

QY 181 NMTNHSFMCCLIKYGLRVNQTNNWTTKQEHFPDN 216

Db 207 NMTNHSFMCCLIKYGLRVNQTNNWTTKQEHFPDN 242

RESULT 11

AAE14633
 ID AAE14633 standard; Protein; 288 AA.

XX
 AC AAE14633;

XX 16-JUL-2002 (first entry)

XX Human B7-1 protein.

XX T cell; CD3; accessory molecule; CD28; cancer; infectious disease;
 KW immunotherapy; human immunodeficiency virus; HIV infection;
 KW cytokine; human; B7-1; CD80.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..34
 FT /label= Signal_peptide
 FT Protein 35..288
 FT /note= "Mature B7-1 protein"
 FT Domain 35..242
 FT /label= Extracellular_domain
 FT Domain 35..138
 FT /note= "Ig V-set domain"
 FT Modified-site 53..55
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 89..91
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 98..100
 FT /note= "Asn is N-glycosylated"
 FT Domain 139..236
 FT /note= "Ig C-set domain"
 FT Modified-site 186..188
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 207..209
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 211..213
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 226..228
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 232..234
 FT /note= "Asn is N-glycosylated"
 FT Domain 243..269
 FT /label= Transmembrane_domain
 FT Domain 270..288
 FT /label= Intracellular_domain
 XX USG352694-B1.
 PN
 XX
 XX
 PD
 XX
 PF 10-MAR-1995; 95US-0403253.
 XX
 XX
 PR 03-JUN-1994; 94US-0253964.
 XX
 PA (GENY) GENETICS INST INC.
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
 XX
 DR WPI; 2002-314696/35.
 DR N-PSDB; AAD27967.
 XX
 PT Inducing T cell population to proliferate, useful in cancer therapy,
 PT comprises activating T cells by contacting T cells in vitro with
 PT immobilized anti-CD3 antibody and stimulating accessory molecule on T
 PT cell surface -
 XX
 XX Example 11; Column 59-62; 71pp; English.
 PS
 XX The invention relates to a method of inducing T cell population to
 CC proliferate for use in therapy comprising activating T cells by
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised
 CC on solid phase surface, and stimulating accessory molecule on T cell
 CC surface in vitro with anti-CD28 antibody, or stimulatory form of
 CC natural ligand for CD28 such as B7-1 or B7-2. The method is useful
 CC for inducing a population of T cells to proliferate in sufficient
 CC numbers for use in therapy e.g., for treating cancer or an infectious
 CC disease. The method can be used to selectively expand the
 CC population of CD28⁺, CD4⁺, CD8⁺, CD28RA⁺ or CD28RO⁺ T cells for
 CC immunotherapy. The T cell population resulting by the method can be
 CC genetically transduced and used for immunotherapy or can be used for in
 CC vitro analysis of infectious agents such as human Immunodeficiency
 CC virus (HIV). Proliferation of a population of CD4⁺ T cells obtained
 CC from an individual infected with HIV can be achieved and the cells
 CC rendered resistant to HIV infection. Following the expansion of the T
 CC cells to sufficient numbers, the expanded T cells are restored to the
 CC individual. Also CD4⁺ T cells expanded by the above mentioned is
 CC useful for treating HIV infection in an individual. A population

CC of tumour-infiltrating lymphocytes can be obtained from an individual
 CC afflicted with cancer and the T cells stimulated to proliferate to
 CC sufficient numbers and restored to the individual. The supernatants from
 CC cultures of T cells expanded from above mentioned method are useful as a
 CC rich source of cytokines and can be used to sustain T cells in vivo or
 CC ex vivo. Stimulating and expanding a population of antigen specific
 CC T cells are useful in therapeutic conditions where it is desirable to
 CC upregulate an immune response. The T cell proliferation occurs in
 CC the absence of exogenous growth factors or accessory cells. The present
 CC sequence is human B7-1 (CD80) transmembrane protein used in the
 CC invention.
 XX
 SQ Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 23; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVKEVATLSGHNVSVEELATRIYWOKEKKMVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVKEVATLSGHNVSVEELATRIYWOKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNETIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLVKADPPTPS 120
 DB 87 YKNETIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLVKADPPTPS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 180
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 206
 QY 181 NMTTNHSPMCLIKYGHRLVNTQTFNNTTKQEHFPDN 216
 DB 207 NMTTNHSPMCLIKYGHRLVNTQTFNNTTKQEHFPDN 242
 RESULT 12
 AAE15829
 ID AAE15829 standard; Protein; 288 AA.
 XX
 XX AAE15829;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX Human co-stimulatory molecule, B7-1 protein.
 DE
 XX Human; vaccine; immunostimulatory molecule; interferon; IFN; therapy;
 KW antigen presentation; vaccine; tumorigenesis; cancer; cytostatic;
 KW antitumour; antibacterial; virucide; fungicide; protozoacide; B7-1.
 XX
 OS Homo sapiens.
 XX
 XX WO200188097-A1.
 PN
 XX 22-NOV-2001.
 PD
 XX 17-MAY-2001; 2001WO-AU00565.
 PF
 XX 17-MAY-2000; 2000AU-0007553.
 PR
 XX (MONU) UNIV MONASH.
 PA
 XX Ralph SJ;
 PI
 XX WPI; 2002-082990/11.
 DR
 XX N-PSDB; AAD25509.
 DR
 XX New composition, useful for treatment and/or prophylaxis of cancer and
 PT tumor, comprises immunostimulatory molecule and animal cells cultured
 PT in presence of interferon to enhance antigen presenting function of the
 PT cells -
 XX
 XX Claim 6; Page 99-100; 127pp; English.
 PS
 XX

CC The present invention relates to a composition of matter comprising an
 CC immunostimulatory molecule and animal cells cultured in the presence of
 CC at least one interferon (IFN) for a time and under conditions sufficient
 CC to enhance the antigen presenting function of the cells. The invention
 CC is used as vaccine. The composition is useful for treatment and/or
 CC prophylaxis of tumorigenesis, cancer, viral, bacterial, fungal and
 CC protozoal infections. The composition which comprises the soluble
 CC immunostimulatory molecule and the cultured animal cells is administered
 CC separately, sequentially or simultaneously to the patient. The present
 CC sequence is human co-stimulatory molecule, B7-1 protein.

XX Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKWKWLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKWKWLTMMSGDMNIWPE 86
 QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTPS 120
 DB 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTPS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLISWLENGEELNAINITVSQDPETELIYAVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLISWLENGEELNAINITVSQDPETELIYAVSSKLD 206
 QY 181 NMTHNSFMCLIKYGHRLRVNQTNNWTKQEHFPDN 216
 DB 207 NMTHNSFMCLIKYGHRLRVNQTNNWTKQEHFPDN 242

RESULT 13

AAM50795
 ID AAM50795 standard; Protein; 288 AA.

AC AAM50795;

XX 23-APR-2002 (first entry)

XX Human B-lymphocyte antigen B7.

XX B-lymphocyte antigen B7; human; T-cell costimulatory molecule;
 KW tumour; sarcoma; lymphoma; melanoma; neuroblastoma; leukaemia;
 KW carcinoma; cancer; metastasis; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..34
 FT /label= Signal_peptide
 FT Protein 35..288
 FT /label= Mature_protein
 FT Domain 35..242
 FT /label= Extracellular_domain
 FT Domain 243..269
 FT /label= Transmembrane_domain
 FT Domain 270..288
 FT /label= Intracellular_domain
 FT Domain 35..138
 FT /label= Ig_V-set_domain
 FT Domain 139..236
 FT /label= Ig_C-set_domain
 FT Modified-site 53..55
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 89..91
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 98..100
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 186..188
 FT /note= "Asn is N-glycosylated"

FT Modified-site 207..209
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 211..213
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 226..228
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 232..234
 FT /note= "Asn is N-glycosylated"

XX US6319709-B1.

PN 20-NOV-2001.

XX 29-NOV-1999; 99US-0450798.

XX 03-NOV-1993; 93US-0147772.

XX 23-SEP-1998; 98US-0159135.

XX (HARD) HARVARD COLLEGE.

XX (DAND) DANA FARBER CANCER INST INC.

XX (UYMA-) UNIV MARYLAND BALTIMORE COUNTY.

XX Ostrand-Rosenberg S, Baskar S, Glimcher LH, Freeman GJ, Nadler LM;

XX WPI; 2002-138256/18.

XX N-PSDB; ABA91632.

XX An isolated mammalian tumour cell transfected with an exogenous nucleic
 PT acid molecule encoding a mammalian B7 molecule which can be used in
 PT methods for treating a patient with a tumour and preventing or
 PT inhibiting metastatic growth -

XX Claim 2; Column 31-34; 24pp; English.

XX The present sequence is that of human B-lymphocyte antigen B7, a
 CC member of the immunoglobulin superfamily with unique expression on
 CC activated and neoplastic cells. The invention provides tumour
 CC cells modified to express a T-cell costimulatory molecule, such as
 CC a CD28 and/or CTLA4 ligand, preferably B-lymphocyte antigen B7.
 CC The tumour cells are modified by transfection with nucleic acid
 CC encoding the T-cell costimulatory molecule, by using an agent which
 CC induces or increases expression of a T-cell costimulatory molecule
 CC on the tumour cell surface or by coupling a T-cell costimulatory
 CC molecule to the tumour cell surface. The tumour cells may be
 CC further modified to express major histocompatibility complex (MHC)
 CC class I and/or class II molecules or have an MHC associated protein,
 CC the invariant chain, inhibited. The modified tumour cells are used
 CC to treat a patient with a tumour, preventing or inhibiting
 CC metastatic spread of a tumour, preventing or inhibiting
 CC recurrence of a tumour. Modification of tumour cells in vivo
 CC makes them capable of triggering a costimulatory signal in T-cells.
 CC The tumour cell is preferably a sarcoma, lymphoma, melanoma,
 CC neuroblastoma, leukaemia or carcinoma.

XX Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKWKWLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKWKWLTMMSGDMNIWPE 86
 QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTPS 120
 DB 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTPS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLISWLENGEELNAINITVSQDPETELIYAVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLISWLENGEELNAINITVSQDPETELIYAVSSKLD 206
 QY 181 NMTHNSFMCLIKYGHRLRVNQTNNWTKQEHFPDN 216

QY 61 YKNETIFDITNNLSIVILALRPSDEGTVECVWLKYEKDAFKREHLAEVTL SVKADFPPTS 120
Db 87 YKNETIFDITNNLSIVILALRPSDEGTVECVWLKYEKDAFKREHLAEVTL SVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAYSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAYSSKLD 206
QY 181 NMTNHSFMCCLKYGHRLRVNOTFNWNTTKOHPFDN 216
Db 207 NMTNHSFMCCLKYGHRLRVNOTFNWNTTKOHPFDN 242

Search completed: January 6, 2003, 14:24:07
Job time : 38 secs

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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:23:30 ; Search time 14 Seconds
(without alignments)
453.954 Million cell updates/sec

Title: US-09-454-651B-23
Sequence: 1 GLSHFCGVHVTKEVKA.....LRVNTFNWNTTKQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1149	100.0	288	2 US-08-147-772-2	Sequence 2, Appli
2	1149	100.0	288	2 US-08-456-104-6	Sequence 6, Appli
3	1149	100.0	288	2 US-08-101-624-23	Sequence 23, Appl
4	1149	100.0	288	2 US-08-751-767A-6	Sequence 6, Appli
5	1149	100.0	288	3 US-08-153-262-2	Sequence 2, Appli
6	1149	100.0	288	3 US-08-479-744A-29	Sequence 29, Appl
7	1149	100.0	288	4 US-08-280-757B-29	Sequence 29, Appl
8	1149	100.0	288	4 US-09-159-135-2	Sequence 2, Appli
9	1149	100.0	288	4 US-08-205-697A-19	Sequence 19, Appl
10	1149	100.0	288	4 US-08-702-525-19	Sequence 19, Appl
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16	1102	95.9	208	4 US-09-460-384-36	Sequence 36, Appl
17	1100	95.7	288	4 US-09-651-200-14	Sequence 14, Appl
18	1050	91.4	208	3 US-08-630-172-15	Sequence 15, Appl
19	1050	91.4	208	4 US-09-375-419-15	Sequence 15, Appl
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21	738	64.2	299	4 US-09-651-200-15	Sequence 15, Appl
22	561	48.8	306	4 US-08-205-697A-17	Sequence 17, Appl
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27	561	48.8	320	4 US-08-702-525-2	Sequence 2, Appli

Sequence 2, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 25, Appl
Sequence 4, Appli
Sequence 31, Appl
Sequence 31, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 65, Appl

561 48.8 320 5 PCT-US95-02576-2
558 48.6 306 2 US-08-147-772-4
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558 48.6 306 2 US-08-101-624-25
558 48.6 306 3 US-08-153-262-4
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558 48.6 306 4 US-09-159-135-4
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311 27.1 200 4 US-08-205-697A-9
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311 27.1 214 5 PCT-US95-02576-11
250.5 21.8 212 4 US-08-702-525-63
250.5 21.8 212 5 PCT-US95-02576-63
250.5 21.8 226 4 US-08-702-525-65

ALIGNMENTS

RESULT 1
US-08-147-772-2
; Sequence 2, Application US/08147772
; Patent No. 5858776

GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
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NAME/KEY: N-linked glycosylation
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FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
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NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
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IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal Of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-147-772-2
Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVKVATLSCGHNVSVEELAQTRIYWQEKKNMVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVKVATLSCGHNVSVEELAQTRIYWQEKKNMVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADPTPS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSKLDP 180
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSKLDP 206
QY 181 NMTNHSFMCCLKYGHRLVQNTFNNTTKQEHFPDN 216
DB 207 NMTNHSFMCCLKYGHRLVQNTFNNTTKQEHFPDN 242
RESULT 2
US-08-456-104-6
Sequence 6, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456.104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-104-6

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATISCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 50
|||||
DB 27 GLSHFCSGVIHVTKEVATISCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 86
|||||
QY 61 YKNTFTDITNLSIVILALRPSDEGTVCYVVKYKDAFKREHLAEVTLVKADFPPTPS 120
|||||
DB 87 YKNTFTDITNLSIVILALRPSDEGTVCYVVKYKDAFKREHLAEVTLVKADFPPTPS 146
|||||
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 180
|||||
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 206
|||||
QY 181 NMTNHSFCLIKYGLHRLVNOTFNWNTTKQEHFPDN 216
|||||
DB 207 NMTNHSFCLIKYGLHRLVNOTFNWNTTKQEHFPDN 242
|||||

RESULT 3
US-08-101-624-23
Sequence 23, Application US/08101624
Patent No. 5942607
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/101,624
FILING DATE: 26-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE: for CD28 T cell surface antigen; transmembrane protein
NAME/KEY: signal sequence

LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.

IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-153-262-2
Query Match 100.0%; Score 1149; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVKVATLSCHGNVSVEELAQTRIYVQKEKKMVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVKVATLSCHGNVSVEELAQTRIYVQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFTPS 120
DB 87 YKNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSDPETELXAVSSKLD 180
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSDPETELXAVSSKLD 206
QY 181 NMTNHSFMCLIKYHLRVNQTFFNNTTKQEHFPDN 216
DB 207 NMTNHSFMCLIKYHLRVNQTFFNNTTKQEHFPDN 242
RESULT 6
US-08-479-744A-29
Sequence 29, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
NAME/KEY: Ig V-set domain

LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-479-744A-29
Query Match 100.0%; Score 1149; DB 3: Length 288;
Best Local Similarity 100.0%; Pred. No. 5,5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYKDKAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYKDKAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAVSSKLDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAVSSKLDF 206
QY 181 NMTTNHSEFMCLIKYGHRLRVNQTFFNNTTKQEHFPDN 216
DB 207 NMTTNHSEFMCLIKYGHRLRVNQTFFNNTTKQEHFPDN 242
RESULT 7
US-08-280-757B-29
Sequence 29, Application us/08280757B
Patent No. 6130316
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-280-757B-29
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVATLSCGHNVSEELAQTRIYQKQKMWLTWMSGDMNIWPE 60
|||||
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSEELAQTRIYQKQKMWLTWMSGDMNIWPE 86
QY 61 YKNRTIFDTNNLSIVILALRPSDEGTTCVWLKYEKDAFKREHLAEVTLVKADFPPTPS 120
|||||
Db 87 YKNRTIFDTNNLSIVILALRPSDEGTTCVWLKYEKDAFKREHLAEVTLVKADFPPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
|||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
QY 181 NMTNHSFMCILIKYGLRVNQTFNNTTKOEHPDN 216
|||||
Db 207 NMTNHSFMCILIKYGLRVNQTFNNTTKOEHPDN 242
RESULT 8
US-09-159-135-2
Sequence 2, Application US/09159135
Patent No. 6149905
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: 34 to 101
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEDMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: WHITMAN, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-09-159-135-2
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTREKVEATVLSGHNVSVEELAQTRIVQKEKKMVLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTREKVEATVLSGHNVSVEELAQTRIVQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNNLSIVILALRPSDEGTGYECVVLKYKEDAFKREHLAEVTLVKADPPTPS 120
DB 87 YKNTIFDITNNLSIVILALRPSDEGTGYECVVLKYKEDAFKREHLAEVTLVKADPPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGBELNAINTTVSQDPETELAVSSKLPD 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGBELNAINTTVSQDPETELAVSSKLPD 206
QY 181 NMTTNHSMCLIKYCHLRVNTQTFNNTTKQEHFPDN 216
DB 207 NMTTNHSMCLIKYCHLRVNTQTFNNTTKQEHFPDN 242
RESULT 9
US-08-205-697A-19
; Sequence 19, Application US/08205697A
; Patent No. 621510
; GENERAL INFORMATION:

APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaolo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-205-697A-19
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCGSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDTNLSIVILALRPSDEGTCEYCVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDTNLSIVILALRPSDEGTCEYCVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCILIKYGHRLVNQTFNNTTKQEHPPDN 216
Db 207 NMTNHSFMCILIKYGHRLVNQTFNNTTKQEHPPDN 242
RESULT 10
US-08-702-525-19
Sequence 19, Application US/08/702525
Patent No. 6294660
GENERAL INFORMATION:
APPLICANT: Sharpe, Sharpe
APPLICANT: Borriello, Francescopaolo
APPLICANT: Freeman, Gordon
APPLICANT: Nadler, Lee
TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
Molecules and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,525
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-525-19
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCGSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDTNLSIVILALRPSDEGTCEYCVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDTNLSIVILALRPSDEGTCEYCVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCILIKYGHRLVNQTFNNTTKQEHPPDN 216
Db 207 NMTNHSFMCILIKYGHRLVNQTFNNTTKQEHPPDN 242
RESULT 11
US-09-450-798-2
Sequence 2, Application US/09450798
Patent No. 6319709
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/450,798
FILING DATE: 29-NOV-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-09-450-798-2
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLSHFCSGVHVTKVEKAVTLSCGHNVSVLELAOTRIYQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVHVTKVEKAVTLSCGHNVSVLELAOTRIYQKEKKMVLTMMSGDMNIWPE 86
Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLVKADPPTPS 146
Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNINTVTSQDPETELXAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNINTVTSQDPETELXAVSSKLD 206
Qy 181 NMTNHSFMCILIKYHLRVNQTFFNNTTKQEHFPDN 216
Db 207 NMTNHSFMCILIKYHLRVNQTFFNNTTKQEHFPDN 242
RESULT 12
US-08-403-253A-2
Sequence 2, Application US/08403253A
Patent No. 6352694
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennett, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-cell
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts

COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/403,253A
 FILING DATE: March 10, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/253,964
 FILING DATE: 3 JUNE 1994
 APPLICATION NUMBER: US 08/073,223
 FILING DATE: 4 JUNE 1993
 APPLICATION NUMBER: US 08/200,947
 FILING DATE: 23 FEB 1994
 APPLICATION NUMBER: US 07/864,805
 FILING DATE: 7 APR 1992
 APPLICATION NUMBER: US 08/247,505
 FILING DATE: 23 MAY 1994
 APPLICATION NUMBER: US 07/864,866
 FILING DATE: 7 APR 1992
 APPLICATION NUMBER: US 08/218,155
 FILING DATE: 25 MAR 1994
 APPLICATION NUMBER: US 07/864,807
 FILING DATE: 7 APR 1992
 APPLICATION NUMBER: US 07/902,467
 FILING DATE: 16 JUNE 1992
 APPLICATION NUMBER: US 07/275,433
 FILING DATE: 23 NOV 1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: RPI-002CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: B cell activation antigen; natural ligand
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
 FEATURE:
 NAME/KEY: signal sequence
 LOCATION: -34 to -1
 IDENTIFICATION METHOD: amino terminal sequencing of
 IDENTIFICATION METHOD: soluble protein
 OTHER INFORMATION: hydrophobic
 FEATURE:
 NAME/KEY: extracellular domain
 LOCATION: 1 to 208
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: transmembrane domain
 LOCATION: 209 to 235
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: intracellular domain
 LOCATION: 236 to 254
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 19 to 21
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence

FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 55 to 57
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 64 to 66
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 152 to 154
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 173 to 175
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 177 to 179
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 192 to 194
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 198 to 200
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: Ig V-set domain
 LOCATION: 1 to 104
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: Ig C-set domain
 LOCATION: 105 to 202
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 PUBLICATION INFORMATION:
 AUTHORS: FREEMAN, GORDON J.
 AUTHORS: FREEDMAN, ARNOLD S.
 AUTHORS: SEGIL, JEFFREY M.
 AUTHORS: LEE, GRACE
 AUTHORS: WHITMAN, JAMES F.
 AUTHORS: NADLER, LEE M.
 TITLE: B7, A New Member Of The Ig Superfamily With
 TITLE: Unique Expression On Activated And Neoplastic B Cells
 JOURNAL: The Journal of Immunology
 VOLUME: 143
 ISSUE: 8
 PAGES: 2714-2722
 DATE: 15-OCT-1989
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
 US-08-403-253A-2
 Query Match 100.0%; Score 1149; DB 4; Length 288;
 Best Local Similarity 100.0%; Pred No. 5,5e-113;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQRIYWKQKMYLTWMSGDMNWIPE 60
 Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQRIYWKQKMYLTWMSGDMNWIPE 86
 QY 61 YKNRTFTDITNNLSIVILALRPDSDEGTTCVWLYKYEKDAFKREHLAEVTLVSKADFTPS 120
 Db 87 YKNRTFTDITNNLSIVILALRPDSDEGTTCVWLYKYEKDAFKREHLAEVTLVSKADFTPS 146


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QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
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Db 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 181 NMTNHSFMCILIKYGHRLRVNOTFNWNTTKQEHFPDN 216
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Db 207 NMTNHSFMCILIKYGHRLRVNOTFNWNTTKQEHFPDN 242
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RESULT 13
US-09-651-200-13
: Sequence 13, Application US/09651200

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Query Match	100.0%	Score 1149;	DB 4;	Length 288;
Best Local Similarity	100.0%	Pred. No. 5.5e-113;		
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Qy	61	YKNRTTFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKEHLEAVTLSVKADFPPTS	120
Db	87	YKNRTTFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKEHLEAVTLSVKADFPPTS	146
Qy	121	ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSDOPTETELYAVSSKLDf	180
Db	147	ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSDOPTETELYAVSSKLDf	206
Qy	181	NMTTNSFMCLLIKYGHILRVNQTFNNNTTKQEHFPD	216
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPCC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-02576-19

Query Match 100.0%; Score 1149; DB 5; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVLHVYKEVKEVATLSCGHNVSVPEELAQTRIYWQEKKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVLHVYKEVKEVATLSCGHNVSVPEELAQTRIYWQEKKKMVLTMMSGDMNIWPE 86

QY 61 YKNTIFDITNNLSIVILALRPSDEGYECVWLKYEKDAFKREHLAETVLSVKADFPTPS 120
Db 87 YKNTIFDITNNLSIVILALRPSDEGYECVWLKYEKDAFKREHLAETVLSVKADFPTPS 146

QY 121 ISDFEPTSNIRRICTSGGFPFPHLSWLENGEELNAINTVSDPETELIYAVSSKLD 180
Db 147 ISDFEPTSNIRRICTSGGFPFPHLSWLENGEELNAINTVSDPETELIYAVSSKLD 206

QY 181 NMTNTNSFMCLIKYGLHVRVQNTFNWNTTKQEHFPDN 216
Db 207 NMTNTNSFMCLIKYGLHVRVQNTFNWNTTKQEHFPDN 242

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized

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US-09-171-945-131

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Best Local Similarity 100.0%; Pred. No. 1.2e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GLSHFCSGVIHVTKEVKVATLSCHNVSVBELAQTRIYWQEKKKMVLTMMSGDMNIWPE	60
Db	27	GLSHFCSGVIHVTKEVKVATLSCHNVSVBELAQTRIYWQEKKKMVLTMMSGDMNIWPE	86
Qy	61	YKNRTIFDITNNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVKADFTPS	120
Db	87	YKNRTIFDITNNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVKADFTPS	146
Qy	121	ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD	180
Db	147	ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD	206
Qy	181	NMTTNHSPMCLIKYGHRLVNOTFNWNTTKQEHFPDN	216
Db	207	NMTTNHSPMCLIKYGHRLVNOTFNWNTTKQEHFPDN	242

Search completed: January 6, 2003, 14:25:51
Job time : 16 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 14:25:11 ; Search time 11 seconds
(without alignments)
372.139 Million cell updates/sec

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Perfect score: 1149
Sequence: 1 GLSHFCGVIHVTKEVKEVA.....LRVNTQFNWNTTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	226	8	US-09-915-789A-21
2	1149	100.0	288	9	US-08-592-711-2
3	1149	100.0	288	9	US-09-896-738-10
4	1149	100.0	288	9	US-09-915-789A-15
5	1149	100.0	288	10	US-09-772-102-14
6	1149	100.0	288	10	US-09-837-867A-19
7	1149	100.0	288	10	US-09-910-174A-5
8	1149	100.0	473	10	US-09-910-059-131
9	1143	99.5	492	10	US-09-845-899A-3
10	1042	90.7	224	10	US-09-955-866-4
11	915	79.6	313	10	US-09-756-983-15
12	743	64.7	292	10	US-09-303-510-2
13	743	64.7	292	10	US-09-303-040-2
14	739	64.3	292	10	US-09-303-510-4
15	739	64.3	292	10	US-09-303-040-4
16	561	48.8	306	10	US-09-837-867A-17
17	561	48.8	320	10	US-09-837-867A-2
18	311	27.1	200	10	US-09-837-867A-9
19	311	27.1	214	10	US-09-837-867A-11

20	200.5	17.4	329	10	US-09-303-510-6	Sequence 6, Appli
21	200.5	17.4	329	10	US-09-303-040-6	Sequence 6, Appli
22	182	15.8	219	9	US-09-915-789A-22	Sequence 22, Appli
23	182	15.8	260	10	US-09-845-899A-5	Sequence 5, Appli
24	182	15.8	323	9	US-09-896-738-11	Sequence 11, Appli
25	182	15.8	323	9	US-09-915-789A-16	Sequence 16, Appli
26	182	15.8	323	10	US-09-955-866-5	Sequence 5, Appli
27	182	15.8	324	10	US-09-910-174A-6	Sequence 6, Appli
28	182	15.8	329	8	US-08-592-711-4	Sequence 4, Appli
29	182	15.8	329	10	US-09-837-867A-23	Sequence 23, Appli
30	182	15.8	351	10	US-09-756-983-18	Sequence 18, Appli
31	161	14.0	302	9	US-09-896-738-13	Sequence 13, Appli
32	161	14.0	302	10	US-09-789-561-136	Sequence 136, App
33	161	14.0	302	10	US-09-955-866-7	Sequence 7, Appli
34	161	14.0	309	10	US-09-910-174A-7	Sequence 7, Appli
35	161	14.0	344	10	US-09-764-853-812	Sequence 812, App
36	160	13.9	241	9	US-09-915-789A-11	Sequence 11, Appli
37	160	13.9	302	9	US-09-915-789A-18	Sequence 18, Appli
38	160	13.9	343	10	US-09-764-853-630	Sequence 630, App
39	160	13.9	345	10	US-09-764-853-810	Sequence 810, App
40	158.5	13.8	480	10	US-09-875-338-5	Sequence 5, Appli
41	156.5	13.6	220	9	US-09-915-789A-23	Sequence 23, Appli
42	156.5	13.6	245	9	US-10-068-215-2	Sequence 2, Appli
43	156.5	13.6	245	12	US-10-002-775-2	Sequence 2, Appli
44	156.5	13.6	290	9	US-10-068-215-4	Sequence 4, Appli
45	156.5	13.6	290	9	US-09-896-913A-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-915-789A-21
; Sequence 21, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match	100.0%;	Score 1149;	DB 9;	Length 226;
Best Local Similarity	100.0%;	Pred. No. 3.4e-86;		
Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIYQWKKMVLTMNSGDMNLWPE	60	
Db	11	GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIYQWKKMVLTMNSGDMNLWPE	70	
QY	61	YKNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSRADFPTPS	120	
Db	71	YKNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSRADFPTPS	130	
QY	121	ISDFEPTSNIRRIICSTSGGFPPEHLWSWLENGEELNAINVTVSQDPETELYAVSSKLD	180	
Db	131	ISDFEPTSNIRRIICSTSGGFPPEHLWSWLENGEELNAINVTVSQDPETELYAVSSKLD	190	
QY	181	NMTNHSFMCCLIKYGLRVNQTNNWNTTKQEHFPDN	216	
Db	191	NMTNHSFMCCLIKYGLRVNQTNNWNTTKQEHFPDN	226	

RESULT 2
US-08-592-711-2
; Sequence 2, Application US/08592711
; Patent No. US20020115214A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennert, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,711
; FILING DATE: 26-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,816
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10-MARCH-1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3-JUNE-1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4-JUNE-1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23-FEB-1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16-JUNE-1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of
; IDENTIFICATION METHOD: soluble protein
; OTHER INFORMATION: hydrophobic

; FEATURE:
; NAME/KEY: extracellular domain
; LOCATION: 1 to 208
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 209 to 235
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: intracellular domain
; LOCATION: 236 to 254
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 19 to 21
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 55 to 57
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 64 to 66
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 152 to 154
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 173 to 175
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 177 to 179
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 192 to 194
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 198 to 200
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig V-set domain
; LOCATION: 1 to 104
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig C-set domain
; LOCATION: 105 to 202
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; PUBLICATION INFORMATION:
; AUTHORS: FREEMAN, GORDON J.
; AUTHORS: FREEDMAN, ARNOLD S.
; AUTHORS: SEGIL, JEFFREY M.
; AUTHORS: LEE, GRACE
; AUTHORS: WHITMAN, JAMES F.
; AUTHORS: NADLER, LEE M.
; TITLE: B7, A New Member Of The Ig Superfamily With

; TITLE: Unique Expression On Activated And Neoplastic B Cells
 ; JOURNAL: The Journal of Immunology
 ; VOLUME: 143
 ; ISSUE: 8
 ; PAGES: 2714-2722
 ; DATE: 15-OCT-1989
 ; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
 US-08-592-711-2

Query Match 100.0%; Score 1149; DB 8; Length 288;
 Best Local Similarity 100.0%; Pred. No. 4.5e-86;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGSGVIHVTKEVATLSCGHNVSVLELAQTRIVYQKEKKMVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGSGVIHVTKEVATLSCGHNVSVLELAQTRIVYQKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKLD 206
 QY 181 NMTTHSFMCILIKYGLHVRVNTFNNTTQEHFPDN 216
 DB 207 NMTTHSFMCILIKYGLHVRVNTFNNTTQEHFPDN 242

RESULT 3
 US-09-896-738-10
 ; Sequence 10, Application US/09896738
 ; Patent No. US20020165347A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox, Michael
 ; APPLICANT: Sullivan, John K.
 ; APPLICANT: Fang, Mei
 ; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
 ; CURRENT APPLICATION NUMBER: US/09/896,738
 ; CURRENT FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: 60/215,645
 ; PRIOR FILING DATE: 2000-06-30
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 288
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-896-738-10

Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 4.5e-86;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGSGVIHVTKEVATLSCGHNVSVLELAQTRIVYQKEKKMVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGSGVIHVTKEVATLSCGHNVSVLELAQTRIVYQKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKLD 206
 QY 181 NMTTHSFMCILIKYGLHVRVNTFNNTTQEHFPDN 216
 DB 207 NMTTHSFMCILIKYGLHVRVNTFNNTTQEHFPDN 242

RESULT 4
 US-09-915-789A-15
 ; Sequence 15, Application US/09915789A
 ; Patent No. US20020168762A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Lieping
 ; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
 ; MOLECULES
 ; FILE REFERENCE: 07039-219001
 ; CURRENT APPLICATION NUMBER: US/09/915,789A
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US 60/220,991
 ; PRIOR FILING DATE: 2000-07-27
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 288
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-915-789A-15

Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 4.5e-86;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGSGVIHVTKEVATLSCGHNVSVLELAQTRIVYQKEKKMVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGSGVIHVTKEVATLSCGHNVSVLELAQTRIVYQKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELAYVSSKLD 206
 QY 181 NMTTHSFMCILIKYGLHVRVNTFNNTTQEHFPDN 216
 DB 207 NMTTHSFMCILIKYGLHVRVNTFNNTTQEHFPDN 242

RESULT 5
 US-09-772-102-14
 ; Sequence 14, Application US/09772102
 ; Patent No. US20020006413A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sobol, Robert, E.
 ; APPLICANT: Shawler, Daniel L.
 ; APPLICANT: Bartholomew, Richard M.
 ; APPLICANT: Carlo, Dennis J.
 ; APPLICANT: Gold, Daniel P.
 ; TITLE OF INVENTION: Genetically Engineered Tumor Cell
 ; TITLE OF INVENTION: Vaccines
 ; FILE REFERENCE: P-SD 4581
 ; CURRENT APPLICATION NUMBER: US/09/772,102
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: US 60/178,498
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/185,335
 ; PRIOR FILING DATE: 2000-02-28
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 288
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-772-102-14

Query Match 100.0%; Score 1149; DB 10; Length 288;
 Best Local Similarity 100.0%; Pred. No. 4.5e-86;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLSHFCSGVTHVTKEVKEVATLSCGHNVSVEEEAQTRIYQWEKKMVLTMMSGDMNIWE	60
Db	27	GLSHFCSGVTHVTKEVKEVATLSCGHNVSVEEEAQTRIYQWEKKMVLTMMSGDMNIWE	86
QY	61	YKNRTIFDITNNLSIVILALRPSDEGYECVWLKYEKDAFKRHEHAEVTLISVKADPPTS	120
Db	87	YKNRTIFDITNNLSIVILALRPSDEGYECVWLKYEKDAFKRHEHAEVTLISVKADPPTS	146
QY	121	ISDFEIPTSIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSQDPETELVAVSSKLPD	180
Db	147	ISDFEIPTSIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSQDPETELVAVSSKLPD	206
QY	181	NMTNHSFMCLIKYGLHRVQNTFNWNTTKOEHPDN	216
Db	207	NMTNHSFMCLIKYGLHRVQNTFNWNTTKOEHPDN	242

RESULT 6

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US-09-837-867A-19
; Sequence 19, Application US/09837867A
; Patent No. US20020098542A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. US20020098542A1el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; FILE REFERENCE: BWI-120CPADV
; CURRENT APPLICATION NUMBER: US/09/837,867A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 08/205,697
; PRIOR FILING DATE: 1994-03-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-837-867A-19

```

RESULT 7

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US-09-910-174A-5
RESOLI /
; Sequence 5, Application US/09910174A
; Patent No. US20020106730A1
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. US20020106730A1 Members of the B7
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 35800/236924

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```

; CURRENT APPLICATION NUMBER: US/09/910,174A
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 288
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-910-174A-5

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RESULT 8

```

US-09-910-059-131
; Sequence 131, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion
US-09-910-059-131

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	Query Match	100.0%;	Score 1149;	DB 10;	Length 473;
	Best Local Similarity	100.0%;	Pred. No. 8.2e-86;		
	Matches 216;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GLSHFCGVIHVTKEVKEVATLSCGHNVSVSEELAAQTRIYYQKEKKMVLTMWSGDMNIWPE	60		
Db	27	GLSHFCGVIHVTKEVKEVATLSCGHNVSVSEELAAQTRIYYQKEKKMVLTMWSGDMNIWPE	86		
QV	61	YKRTI IDITNNI STVIALRPSPDEGTVECVTKYRKDAFKREHIAEVTTISVAKDEFTPS	120		

Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTVSQDPETELYAVSSKLDLF 180
Db 147 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTVSQDPETELYAVSSKLDLF 206
Qy 181 NMTNHSFMCILKYGHLRVNQTFFNNTTKQEHFPD 216
Db 207 NMTNHSFMCILKYGHLRVNQTFFNNTTKQEHFPD 242

RESULT 9

US-09-845-899A-3
; Sequence 3, Application US/09845899A
; Patent No. US20020147326A1
; GENERAL INFORMATION:
; APPLICANT: CHAIKIN, MARGERY ANN
; APPLICANT: LYN, SALLY DOREEN PATRICIA
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES
; FILE REFERENCE: P50496
; CURRENT APPLICATION NUMBER: US/09/845,899A
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/202,346
; PRIOR FILING DATE: 1999-01-13
; PRIOR FILING DATE: 1997-02-19
; PRIOR FILING DATE: 1997-02-19
; PRIOR FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 492
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-845-899A-3

Query Match 99.5%; Score 1143; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 2.6e-85;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWKQEKKMWLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWKQEKKMWLTMMSGDMNIWPE 86
Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTVSQDPETELYAVSSKLDLF 180
Db 147 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTVSQDPETELYAVSSKLDLF 206
Qy 181 NMTNHSFMCILKYGHLRVNQTFFNNTTKQEHFPD 215
Db 207 NMTNHSFMCILKYGHLRVNQTFFNNTTKQEHFPD 241

RESULT 10

US-09-955-866-4
; Sequence 4, Application US/09955866
; Patent No. US20020107363A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Holst, Paige
; APPLICANT: Yoshinaga, Steven Kiyoshi
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
; FILE REFERENCE: 00.759-A
; CURRENT APPLICATION NUMBER: US/09/955,866

; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,867
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-866-4

Query Match 90.7%; Score 1042; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e-77;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWKQEKKMWLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWKQEKKMWLTMMSGDMNIWPE 86
Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTVSQDPETELYAVSSKLDLF 180
Db 147 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTVSQDPETELYAVSSKLDLF 206
Qy 181 NMTNHSFMCILKYGHLR 198
Db 207 NMTNHSFMCILKYGHLR 224

RESULT 11

US-09-756-983-15
; Sequence 15, Application US/09756983
; Patent No. US20020122818A1
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion constructs with human and bacterial sequences
US-09-756-983-15

Query Match 79.6%; Score 915; DB 10; Length 313;
Best Local Similarity 100.0%; Pred. No. 4.3e-67;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWKQEKKMWLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWKQEKKMWLTMMSGDMNIWPE 86
Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTVSQDPETELYAVS 175


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Db 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVS 201
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RESULT 12
US-09-303-510-2
; Sequence 2, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisison, Ellen W.
; APPLICANT: Hash, Stephen M.
; APPLICANT: Choi, InSoo
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides
; FILE REFERENCE: 54954
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-2

Query Match 64.7%; Score 743; DB 10; Length 292;
Best Local Similarity 63.3%; Pred. No. 3.3e-53;
Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYQKEKKMVLTMMSGDMNIWPEY 61
Db 28 LFYFCGIIQVKNKTVEEAVLSCDYNISTKELTEIRIYQKDDVMVAVMSGKVQWPKY 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADFPPTSI 121
Db 88 KNRTFTVDNHSIVIMALRLSDNGKYTCIIQKIEGSKYVKHLTSVMLLVRAFPVPSI 147
QY 122 SDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDPN 181
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QY 182 MTNHSFCLIKYGHRLVQNTFNWNTTQOEHPDN 216
Db 208 MTNHSFCLVKYGNLLVSQIFNQ--KSEPQPSN 240

RESULT 14
US-09-303-510-4
; Sequence 4, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisison, Ellen W.
; APPLICANT: Hash, Stephen M.
; APPLICANT: Choi, InSoo
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides
; FILE REFERENCE: 54954
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-4

Query Match 64.3%; Score 739; DB 10; Length 292;
Best Local Similarity 62.8%; Pred. No. 7e-53;
Matches 135; Conservative 34; Mismatches 44; Indels 2; Gaps 1;

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QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADFPPTSI 121
Db 88 KNRTFTVDNHSIVIMALRLSDNGKYTCIIQKIEGSKYVKHLTSVMLLVRAFPVPSI 147
QY 122 SDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDPN 181
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QY 182 MTNHSFCLIKYGHRLVQNTFNWNTTQOEHPDN 216
Db 208 MTNHSFCLVKYGNLLVSQIFNQ--KSEPQPSN 240

RESULT 15
US-09-303-040-4
; Sequence 4, Application US/09303040
; Patent No. US20020051792A1
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
; TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof
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Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYQKEKKMVLTMMSGDMNIWPEY 61
Db 28 LFYFCGIIQVKNKTVEEAVLSCDYNISTKELTEIRIYQKDDVMVAVMSGKVQWPKY 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADFPPTSI 121
Db 88 KNRTFTVDNHSIVIMALRLSDNGKYTCIIQKIEGSKYVKHLTSVMLLVRAFPVPSI 147
QY 122 SDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDPN 181
Db 148 TDLGNPSHNIRKIMCLTSGGPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDEN 207
QY 182 MTNHSFCLIKYGHRLVQNTFNWNTTQOEHPDN 216
Db 208 MTNHSFCLVKYGNLLVSQIFNQ--KSEPQPSN 240

RESULT 14
US-09-303-510-4
; Sequence 4, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisison, Ellen W.
; APPLICANT: Hash, Stephen M.
; APPLICANT: Choi, InSoo
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides
; FILE REFERENCE: 54954
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-4

Query Match 64.3%; Score 739; DB 10; Length 292;
Best Local Similarity 62.8%; Pred. No. 7e-53;
Matches 135; Conservative 34; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYQKEKKMVLTMMSGDMNIWPEY 61
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QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADFPPTSI 121
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Db 148 TDLGNPSHNIRKIMCLTSGGPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDEN 207
QY 182 MTNHSFCLIKYGHRLVQNTFNWNTTQOEHPDN 216
Db 208 MTNHSFCLVKYGNLLVSQIFNQ--KSEPQPSN 240

RESULT 15
US-09-303-040-4
; Sequence 4, Application US/09303040
; Patent No. US20020051792A1
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
; TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof
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; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 292
; TYPE: PRT
; ORGANISM: feline CD80
US-09-303-040-4

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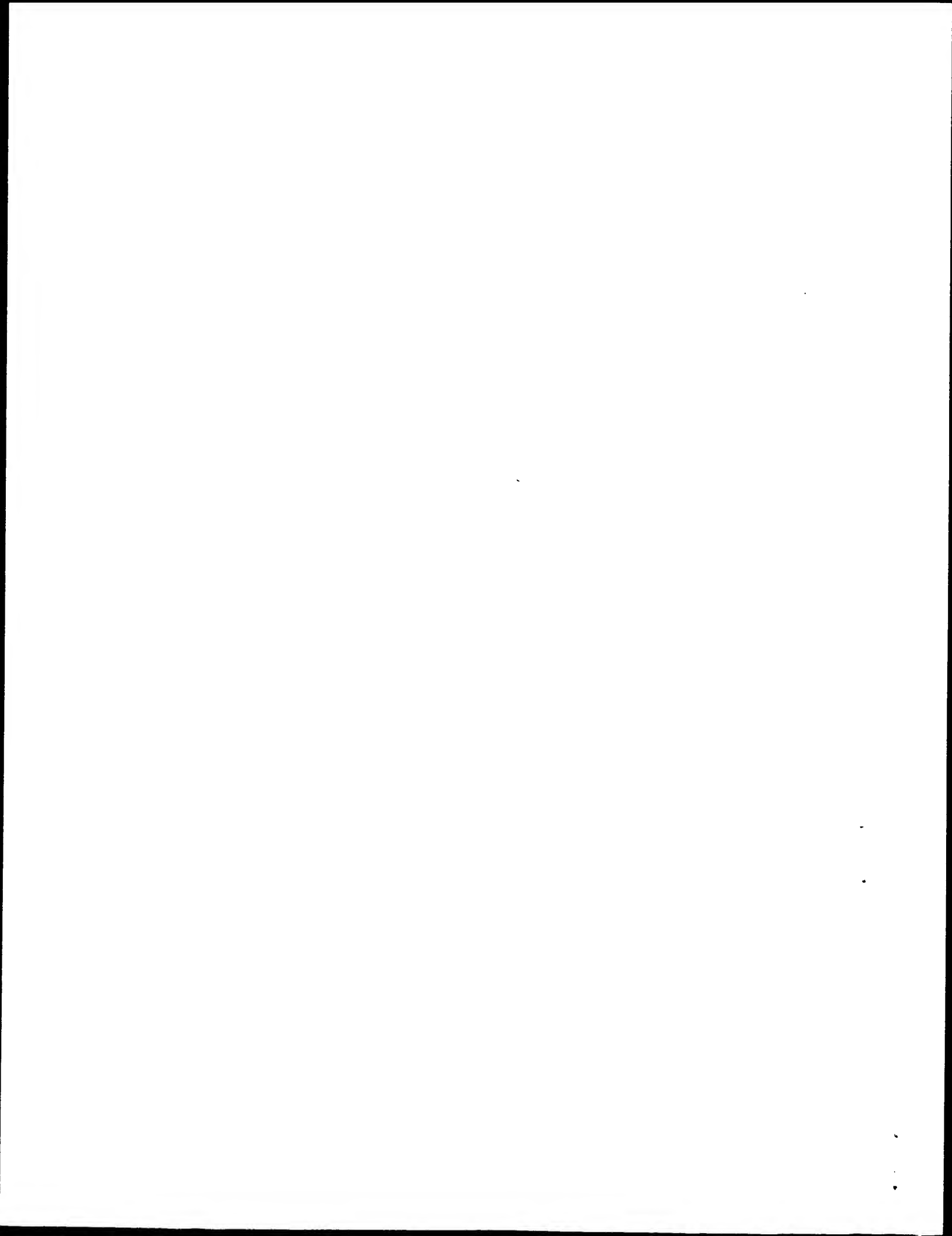
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Query Match      64.3%; Score 739; DB 10; Length 292;
Best Local Similarity 62.8%; Pred. No. 7e-53;
Matches 135; Conservative 34; Mismatches 44; Indels 2; Gaps 1;

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Qy  62 KNRTITDNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLISKADPTPSI 121
Db  88 KNRTFTDVTNHSIVIMALRLSDNGKYTCIIQKIQKGYKVKHLTSVMLLVRADEFVPSI 147
Qy  122 SDFEITPSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 181
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Job time : 12 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:24:10 ; Search time 143 Seconds

(without alignments)
973.863 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

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Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	216	8 US-08-459-766B-8	Sequence 8, Appli
2	1149	100.0	216	18 US-09-454-651B-23	Sequence 23, Appl
3	1149	100.0	216	19 US-09-569-164A-8	Sequence 8, Appli
4	1149	100.0	226	1 PCT-US01-41430-21	Sequence 21, Appl
5	1149	100.0	226	23 US-09-915-789A-21	Sequence 21, Appl
6	1149	100.0	248	1 PCT-US01-06769-12	Sequence 12, Appl

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1 PCT-US01-41430-15
2 PCT-US02-09671-1947
3 PCT-US02-09671-1948
4 PCT-US02-09671-1949
5 PCT-US02-09671-1950
6 PCT-US02-09671-1951
7 PCT-US02-09671-1952
8 PCT-US02-09671-1955
9 PCT-US02-09671-1956
10 PCT-US02-09671-1958
11 PCT-US02-09671-1961
12 PCT-US02-09671-1962
13 PCT-US02-09671-1966
14 PCT-US02-09671-1967
15 PCT-US02-09671-1968
16 PCT-US02-09671-1969
17 PCT-US02-09671-1970
18 US-07-751-306C-2
19 US-08-109-393A-29
20 US-08-147-773-6
21 US-08-280-757-29
22 US-08-435-816A-2
23 US-08-453-386-2
24 US-08-453-386A-2
25 US-08-592-711-2
26 US-09-183-055-2
27 US-09-206-132-6
28 US-09-277-575-2
29 US-09-349-915A-2
30 US-09-349-915B-2
31 US-09-350-202-2
32 US-09-368-581-6
33 US-09-425-516-29
34 US-09-425-762-29
35 US-09-522-206-2
36 US-09-522-206B-2
37 US-09-553-865-2
38 US-09-565-316A-2
39 US-09-620-461-5

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ALIGNMENTS

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RESULT 1
US-08-459-766B-8
; Sequence 8, Application US/08459766B
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
; FILE REFERENCE: 30436.11US04
; CURRENT APPLICATION NUMBER: US/08/459,766B
; CURRENT FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/498,949
; PRIOR FILING DATE: 1990-03-26
; PRIOR APPLICATION NUMBER: 07/547,980
; PRIOR FILING DATE: 1990-07-02
; PRIOR APPLICATION NUMBER: 07/722,101
; PRIOR FILING DATE: 1991-06-27
; PRIOR APPLICATION NUMBER: 08/219,200
; PRIOR FILING DATE: 1994-03-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Freeman, Gordon J.
; AUTHORS: Freedman, Arnold S.

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; AUTHORS: Segil, Jeffrey M.
; AUTHORS: Lee, Grace
; AUTHORS: Whitman, James F.
; AUTHORS: Nadler, Lee M.
; TITLE: B7, A NEW MEMBER OF THE Ig SUPERFAMILY WITH UNIQUE
; TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
; JOURNAL: J. Immunol.
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 1989-10-15
; RELEVANT RESIDUES: 1 TO 216
US-08-459-766B-8

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Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 YKNRTIFDTNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
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DB 121 ISDFEPTNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 180
QY 181 NMTNHSFMCCLKYGHRLVNOTFNNTTKQEHFPDN 216
DB 181 NMTNHSFMCCLKYGHRLVNOTFNNTTKQEHFPDN 216

RESULT 2

US-09-454-651B-23
; Sequence 23, Application US/09454651B
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; Ledbetter, Jeffrey A.
; Damle, Nitin K.
; Brady, William
; Wallace, Philip M.
; TITLE OF INVENTION: CIL4/CD28Ig HYBRID FUSION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mandel & Adriano
; STREET: 35 N. Arroyo Parkway, Suite 60
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454.651B
; FILING DATE: 06-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/228,208
; FILING DATE: 15-APR-1994
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470

; REFERENCE/DOCKET NUMBER: 30436.30USD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 626 395-7801
; TELEFAX: 626 395-0694
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 216 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-454-651B-23

Query Match 100.0%; Score 1149; DB 18; Length 216;
Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 YKNRTIFDTNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
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RESULT 3

US-09-569-164A-8
; Sequence 8, Application US/09569164A
; GENERAL INFORMATION:
; APPLICANT: LINSLEY, PETER S. ET AL.
; TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/569,164A
; CURRENT FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 07/547,980
; PRIOR FILING DATE: 1990-07-02
; PRIOR APPLICATION NUMBER: 07/722,101
; PRIOR FILING DATE: 1991-06-27
; PRIOR APPLICATION NUMBER: 08/219,200
; PRIOR FILING DATE: 1994-03-29
; PRIOR APPLICATION NUMBER: 08/459,766
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Freeman, Gordon J.
; AUTHORS: Freedman, Arnold S.
; AUTHORS: Segil, Jeffrey M.
; AUTHORS: Lee, Grace
; AUTHORS: Whitman, James F.
; AUTHORS: Nadler, Lee M.
; TITLE: B7, A NEW MEMBER OF THE Ig SUPERFAMILY WITH UNIQUE
; TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
; JOURNAL: J. Immunol.
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 1989-10-15


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; RELEVANT RESIDUES: 1 TO 216
US-09-569-164A-8

Query Match      100.0%; Score 1149; DB 19; Length 216;
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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYEKDAFKREHLAEVTLVSKADFPPTS 120
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QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
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QY 181 NMTNHSFMCCLKYGHRLRVNQTENNNTTKQEHFPDN 216
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Db 181 NMTNHSFMCCLKYGHRLRVNQTENNNTTKQEHFPDN 216

RESULT 4
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; Sequence 21, Application PC/TUS0141430
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219W01
; CURRENT APPLICATION NUMBER: PCT/US01/41430
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/220,991
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-41430-21

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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 70

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYEKDAFKREHLAEVTLVSKADFPPTS 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 71 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYEKDAFKREHLAEVTLVSKADFPPTS 130

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 190

QY 181 NMTNHSFMCCLKYGHRLRVNQTENNNTTKQEHFPDN 216
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 191 NMTNHSFMCCLKYGHRLRVNQTENNNTTKQEHFPDN 226

RESULT 5
US-09-915-789A-21
; Sequence 21, Application US/09915789A
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219001
```

```
; CURRENT APPLICATION NUMBER: US/09/915.789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match      100.0%; Score 1149; DB 23; Length 226;
Best Local Similarity 100.0%; Pred. No. 8.9e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 11 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 70

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYEKDAFKREHLAEVTLVSKADFPPTS 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 71 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYEKDAFKREHLAEVTLVSKADFPPTS 130

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 190

QY 181 NMTNHSFMCCLKYGHRLRVNQTENNNTTKQEHFPDN 216
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 191 NMTNHSFMCCLKYGHRLRVNQTENNNTTKQEHFPDN 226

RESULT 6
PCT-US01-06769-12
; Sequence 12, Application PC/TUS0106769
; GENERAL INFORMATION:
; APPLICANT: Mayo Medical Ventures
; TITLE OF INVENTION: hb7-H2, A NOVEL CO-STIMULATORY MOLECULE
; FILE REFERENCE: 07039-202W01
; CURRENT APPLICATION NUMBER: PCT/US01/06769
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/186,519
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-06769-12

Query Match      100.0%; Score 1149; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 86

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYEKDAFKREHLAEVTLVSKADFPPTS 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYEKDAFKREHLAEVTLVSKADFPPTS 146

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206

QY 181 NMTNHSFMCCLKYGHRLRVNQTENNNTTKQEHFPDN 216
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 207 NMTNHSFMCCLKYGHRLRVNQTENNNTTKQEHFPDN 242
```



```
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1949
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1949
```

```
Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
|||||
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
|||||

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 120
|||||
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 146
|||||

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
|||||
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
|||||

QY 181 NMTNHSFMCILIKYGHRLVQNQTFFNNTTKQEHFPDN 216
|||||
DB 207 NMTNHSFMCILIKYGHRLVQNQTFFNNTTKQEHFPDN 242
|||||
```

```
RESULT 11
PCT-US02-09671-1950
; Sequence 1950, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1950
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1950
```

```
Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
|||||
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
|||||

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 120
|||||
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 146
|||||

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
|||||
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
|||||

QY 181 NMTNHSFMCILIKYGHRLVQNQTFFNNTTKQEHFPDN 216
|||||
DB 207 NMTNHSFMCILIKYGHRLVQNQTFFNNTTKQEHFPDN 242
|||||
```

```
RESULT 12
PCT-US02-09671-1951
; Sequence 1951, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1951
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1951
```

```
Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 60
|||||
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQKEKKMVLTMMSGDMNIWPE 86
|||||

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 120
|||||
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 146
|||||

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
|||||
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
|||||

QY 181 NMTNHSFMCILIKYGHRLVQNQTFFNNTTKQEHFPDN 216
|||||
DB 207 NMTNHSFMCILIKYGHRLVQNQTFFNNTTKQEHFPDN 242
|||||
```

RESULT 13


```
PCT-US02-09671-1952
; Sequence 1952, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1952
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1952
```

```
Query Match      100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 60
   |||||||
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 86
   |||||||

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
   |||||||
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146
   |||||||

QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
   |||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
   |||||||

QY 181 NMTTNHSEFCLIKYGHRLVNOTFNNTTKQEHFPDN 216
   |||||||
Db 207 NMTTNHSEFCLIKYGHRLVNOTFNNTTKQEHFPDN 242
   |||||||
```

```
RESULT 14
PCT-US02-09671-1955
; Sequence 1955, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1955
```

```
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1955

Query Match      100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 60
   |||||||
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 86
   |||||||

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
   |||||||
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146
   |||||||

QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
   |||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
   |||||||

QY 181 NMTTNHSEFCLIKYGHRLVNOTFNNTTKQEHFPDN 216
   |||||||
Db 207 NMTTNHSEFCLIKYGHRLVNOTFNNTTKQEHFPDN 242
   |||||||
```

```
RESULT 15
PCT-US02-09671-1956
; Sequence 1956, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1956
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1956
```

```
Query Match      100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 60
   |||||||
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 86
   |||||||

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
   |||||||
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146
   |||||||

QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
   |||||||
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
   |||||||

QY 181 NMTTNHSEFCLIKYGHRLVNOTFNNTTKQEHFPDN 216
   |||||||
```


us-09-454-651b-23.rapm

Tue Jan 7 09:21:48 2003

Db 207 NMTNHSFMCCLKYGHLLRVNQTFFNWTTKQEHFPDN 242

Search completed: January 6, 2003, 14:28:21
Job time : 145 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 14:23:10 ; Search time 21 Seconds

(without alignments)
988.811 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCGVIHVTKEVKEVA.....LRVNTQFNNTTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	A45803	B-cell-restricted
2	1085	94.4	289	G00031	B7 protein - red-c
3	738	64.2	299	I46690	CD80 precursor - r
4	601.5	52.3	321	I54766	B-lymphocyte activ
5	561	48.8	309	I49503	B-lymphocyte activ
6	185	16.1	275	JC7604	CD86 spliced varia
7	182	15.8	329	A48754	B7-2 antigen - hum
8	152	13.2	309	I49522	gene B7-2 protein
9	140.5	12.2	330	I46691	CD86 precursor - r
10	133.5	11.6	583	I39428	alcam - human
11	129	11.2	221	Q0BE48	BARF1 protein - hu
12	127	11.1	526	S70587	butyrophilin precu
13	122.5	10.7	588	JH0506	adhesion molecule
14	122.5	10.7	588	A45254	surface glycoprote
15	120.5	10.5	509	JC5288	SHP substrate-1 pr
16	120.5	10.5	513	JC5289	SHP substrate-1 pr
17	118	10.3	487	S65133	butyrophilin - mou
18	116.5	10.1	1088	IJXLNL	neural cell adhesi
19	115	10.0	761	IJHUNG	neural cell adhesi
20	112.5	9.8	725	JE0099	DM-GRASP precursor
21	110.5	9.6	587	JH0464	cell surface glyco
22	109.5	9.5	646	I38049	neural cell adhesi
23	109.5	9.5	853	IJBONC	butyrophilin - bov
24	109	9.5	526	A37821	protein-tyrosine-p
25	109	9.5	2029	TDPLK	protein-tyrosine k
26	108	9.4	871	I48696	protein-tyrosine k
27	108	9.4	881	I48697	hypothetical prote
28	107.5	9.4	5175	T20992	hemocentin precurs
29	107.5	9.4	5198	T43290	

ALIGNMENTS

RESULT 1

A45803

B-cell-restricted antigen B7 precursor - human

N:Alternate names: B-lymphocyte activation antigen B7

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999

C:Accession: I54495; A45803

R:Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.

Immunogenetics 36, 175-181, 1992

A:Title: Genomic organization and chromosomal location of the human gene encoding the

A:Reference number: I54495; MUID:92307753; PMID:1377173

A:Accession: I54495

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-288 <RES>

A:Cross-references: GB:M83077; NID:g179327; PIDN:AAA58390.1; PID:g179329

R:Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.

J. Immunol. 143, 2714-2722, 1989

A:Title: B7, a new member of the Ig superfamily with unique expression on activated a

A:Reference number: A45803; MUID:90010147; PMID:2794510

A:Accession: A45803

A:Molecule type: mRNA

A:Residues: 1-288 <FRE>

A:Cross-references: GB:M27533; NID:g184680; PIDN:AAA36045.1; PID:g306916

C:Genetics:

A:Gene: GDB:CD80; CD28LG1; CD28

A:Cross-references: GDB:251792; OMIM:112203

A:Map position: 3q13.3-3q21

A:Introns: 34/1; 140/1; 234/1; 266/1

C:Superfamily: B-lymphocyte restricted antigen B7

C:Keywords: transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:248-264/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 1149; DB 2; Length 288;

Best Local Similarity 100.0%; Pred. No. 2e-85; 0; Gaps 0;

Matches 216; Conservative 0; Mismatches 0; Indels 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIVYQKEKKMVLTMMSGDMNTWPE 60

Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIVYQKEKKMVLTMMSGDMNTWPE 86

QY 61 YKNTTFDITNNLSIVLALRPDSDEGTCECVLKYKDAFKREHLAEVTLVSKADFTTTPS 120

Db 87 YKNTTFDITNNLSIVLALRPDSDEGTCECVLKYKDAFKREHLAEVTLVSKADFTTTPS 146

QY 121 ISDFEPTSNIRRICSTSGGFPPEPHLSWLENGLNAINTTVSQDPETELIYAVSSKLDF 180

Db 147 ISDFEPTSNIRRICSTSGGFPPEPHLSWLENGLNAINTTVSQDPETELIYAVSSKLDF 206

QY 181 NMTNHSFMCILIKYGHILRVNQTFNNTTKQEHFPDN 216

|||||

Db 207 NMTNHSFMCILIKYGHRLRVNQTFNNWTTKQEHFPDN 242

RESULT 2
G00031
B7 protein - red-crowned mangabey (fragment)
C:Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C:Accession: G00031
R:Villinger, F.J.
submitted to the EMBL Data Library, January 1995
A:Reference number: G00217
A:Accession: G00031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-289 <VIL>
A:Cross-references: EMBL:U19833; NID:g644783; PIDN:AAA86700.1; PID:g644784
C:Genetics:
A:Gene: B7
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 94.4%; Score 1085; DB 2; Length 289;
Best Local Similarity 95.3%; Pred. No. 3e-80;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVHVTKEVATLSCGHNVSVVEELAQTRIVYQKEKKMVLTMMSGDMNIWPEY 61
|||||
Db 28 LSHFCSGVHVTKEVATLSCGHNVSVVEELAQTRIVYQKEKKMVLTMMSGDMNIWPEY 87
|||||

QY 62 KNTIFDITNNLSIVILALRPSDEGYECVVLKYKDAKREHLAEVTLVSKADFTPTSI 121
|||||
Db 88 KNTIFDITNNLSIVILALRPSDEGYECVVLKYKDAKREHLAEVTLVSKADFTPTSI 147
|||||

QY 122 SFEIPTSNIIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDEN 181
|||||
Db 148 TFEIPTSNIIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDEN 207
|||||

QY 182 MTNHSFMCILIKYGHRLRVNQTFNNWTTKQEHFPDN 216
|||||
Db 208 MTNHSFMCILIKYGHRLRVNQTFNNWTTKQEHFPDN 242
|||||

RESULT 3
146690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: 146690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A:Reference number: 146689; MUID:95369849; PMID:7642234
A:Accession: 146690
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: GB:D49843; NID:g755096; PIDN:BAA08643.1; PID:g755097
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 64.2%; Score 738; DB 2; Length 299;
Best Local Similarity 63.9%; Pred. No. 3.2e-52;
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

QY 4 HFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIVYQKEKKMVLTMMSGDMNIWPEYKN 63
|||||
Db 29 HFSGISQVTSVKEMAALSDYNISIDELAMRIYQKQDMQVLIISGQVEVWPEYKN 88
|||||

QY 64 RTIFDITNNLSIVILALRPSDEGYECVVLKYKDAKREHLAEVTLVSKADFTPTPSID 123
|||||
Db 89 RTFDPDITNNLSIVILALRPSDEGYECVVLKYKDAKREHLAEVTLVSKADFTPTPSID 148
|||||

QY 124 FEIPTSNIIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDEN 183
|||||

Db 149 IGHPDPNVKIRCSASGGFPEPRLAWMEDGEELNAVNTVDQDLDTELYSVSSSELDFNVT 208

QY 184 TNHSFMCILIKYGHRLRVNQTFNNWTTKQE 211
|||||
Db 209 NNHSIVCLIKYGELSVSQIFPWSKPKQE 236
|||||

RESULT 4
154766
B-lymphocyte activation antigen 7-1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C:Accession: 154766
R:Judge, T.A.; Liu, M.; Christensen, P.J.; Fak, J.J.; Turka, L.A.
Int. Immunol. 7, 171-178, 1995
A:Title: Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural and funct
A:Reference number: 154766; MUID:95252184; PMID:7537533
A:Accession: 154766
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-321 <RES>
A:Cross-references: EMBL:U05593; NID:g453381; PIDN:AAA80154.1; PID:g453382
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 52.3%; Score 601.5; DB 2; Length 321;
Best Local Similarity 54.4%; Pred. No. 3.6e-41;
Matches 112; Conservative 35; Mismatches 58; Indels 1; Gaps 1;

QY 1 GLSHFCSGVI-HVTKEVATLSCGHNVSVVEELAQTRIVYQKEKKMVLTMMSGDMNIW 59
|||||
Db 31 GLLISSGIVGVQSVKREKALLSCDYKFCSEQSIHRIYQKHDKMVLVSIQVPEVWP 90
|||||

QY 60 EYKNRTIFDITNNLSIVILALRPSDEGYECVVLKYKDAKREHLAEVTLVSKADFTPT 119
|||||
Db 91 KYKNRTVYDIANNYSFLLGLILSDRGTYTCVVQRYEGGSYVVKHLTTVVELSVRADFPPT 150
|||||

QY 120 SIDSFEIPTSNIIRRICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 179
|||||
Db 151 NITEYGNPSADIKRITCFASGFPKPLSLWLENGLINGINTTISQDPESELYTSSOLD 210
|||||

QY 180 FNMVTNHSFMCILIKYGHRLRVNQTFNW 205
|||||
Db 211 FNATYDHFIDCFIEYGDVHVSQNFNW 236
|||||

RESULT 5
149503
B-lymphocyte activation antigen 7 precursor - mouse
N:Alternate names: MB7-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C:Accession: 149503; S17291; I49521
R:Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A:Reference number: 149503; MUID:93307789; PMID:7686531
A:Accession: 149503
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:L12589; NID:g293299; PIDN:AAA37240.1; PID:g293301
R:Freeman, G.J.; Gray, G.S.; Glimm, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Finge
J. Exp. Med. 174, 625-631, 1991
A:Title: Structure, expression, and T cell costimulatory activity of the murine homol
A:Reference number: S17291; MUID:91341422; PMID:1714935
A:Accession: S17291
A:Molecule type: mRNA
A:Residues: 1-274, 'R', 279-309 <PRE>
A:Cross-references: EMBL:X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112
R:Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Uede, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A:Title: Identification of an alternatively spliced form of the murine homologue of B
A:Reference number: 149521; MUID:94220123; PMID:7513163

A:Accession: I49511
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-143,238-274,'R',279-309 <RE2>
A:Cross-references: GB:D16220; NID:g5051118; PIDN:BAA03748.1; PID:g994769
C:Genetics:
A:Gene: B7
A:Introns: 37/1; 143/1; 237/1; 275/1
A:Superfamily: B-lymphocyte restricted antigen B7
C:Keywords: alternative splicing

Query Match 48.8%; Score 561; DB 2; Length 309;
Best Local Similarity 50.7%; Pred. No. 6.5e-38;
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY 12 VTKVEKATLSCGHNVSEELAQTRIVYQKEKKNVLTMMSGDMNIWPEYKKNRTIFDI 71
DB 42 LSKSVKDKVLLPCRYNSPHEDESEDRIVYQKHDKVSVIAGKLVWPEYKKNRTLYDNT- 100
QY 72 NLSIVILALRPSDEGTVECVLYKEDAFKREHLAEVTLVSVKADFTPTPSISDFEIPTSNI 131
DB 101 TYSLIITGLVSDRGYSYCVQKRGTYEVKHLALVLSINAKADFTPTNITESGNPSADT 160
QY 132 RRTICSTSGGFPPLHLSWLENGEELNAINTVSQDPETELYAVSSKLDNFMTTNHSMCL 191
DB 161 KRITCFASGGFPKPRFSLWLENGEELPGINTTISQDPESELYTSSQLDFTNRNHTIKCL 220
QY 192 IKYGLHVRNQTFFNMNTTQKHFPDN 216
DB 221 IKYGDHVSDEFTWEKPPEDP-PDS 244

RESULT 6
JC7604
CD86 spliced variant CD86 deltaTM isoform - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7604
R:Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A:Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A:Reference number: JC7604; MUID:21092744; PMID:11162656
A:Accession: JC7604
A:Molecule type: mRNA
A:Residues: 1-275 <MAG>
A:Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
C:Genetics:
A:Gene: cd86deltaTM
C:Keywords: immune response

Query Match 16.1%; Score 185; DB 2; Length 275;
Best Local Similarity 27.4%; Pred. No. 1.2e-07;
Matches 165; Conservative 42; Mismatches 78; Indels 52; Gaps 12;

QY 18 EVATLSC---GHNVSVEELAQTRIVYQKEKKNVLTMM---SGDMNIWPEYKKNRTIFDI 69
DB 28 ETADLPQCFANSONQSLSLV---VFQDQENLVNEVLGKEKFDVSHSKYMGRTSFD- 83
QY 70 TNNLSIVILALRPSDEGTVECVLYKEDAFKREHLAEVTLVSVKADFTPTPSISDFEIPTS 129
DB 84 SDSWTLRLHNLQIKDKGLQYIIHKKPTGMIRIHMNSSELSVLANSFQPEI----VPIS 139
QY 130 NIR-----RIICSTSGGFPPEP-HLSWLENGEELNAINTV-----SQDPETELYAVS 175
DB 140 NITENVYINLTCSHIGYPEPKMSVL-----LRTKSTIEYDGMOKSDQNVTELYDVS 194
QY 176 SKLDF---NMTNHSFMCILIKYGLHVRNQ---TFNWNNTKOE-----HFPD 215
DB 195 ISLSVSFDPVTSNMTIFCILETDKTRLSSPFSIGTNTMERESQTKKREKIHPE 251

RESULT 7
A48754

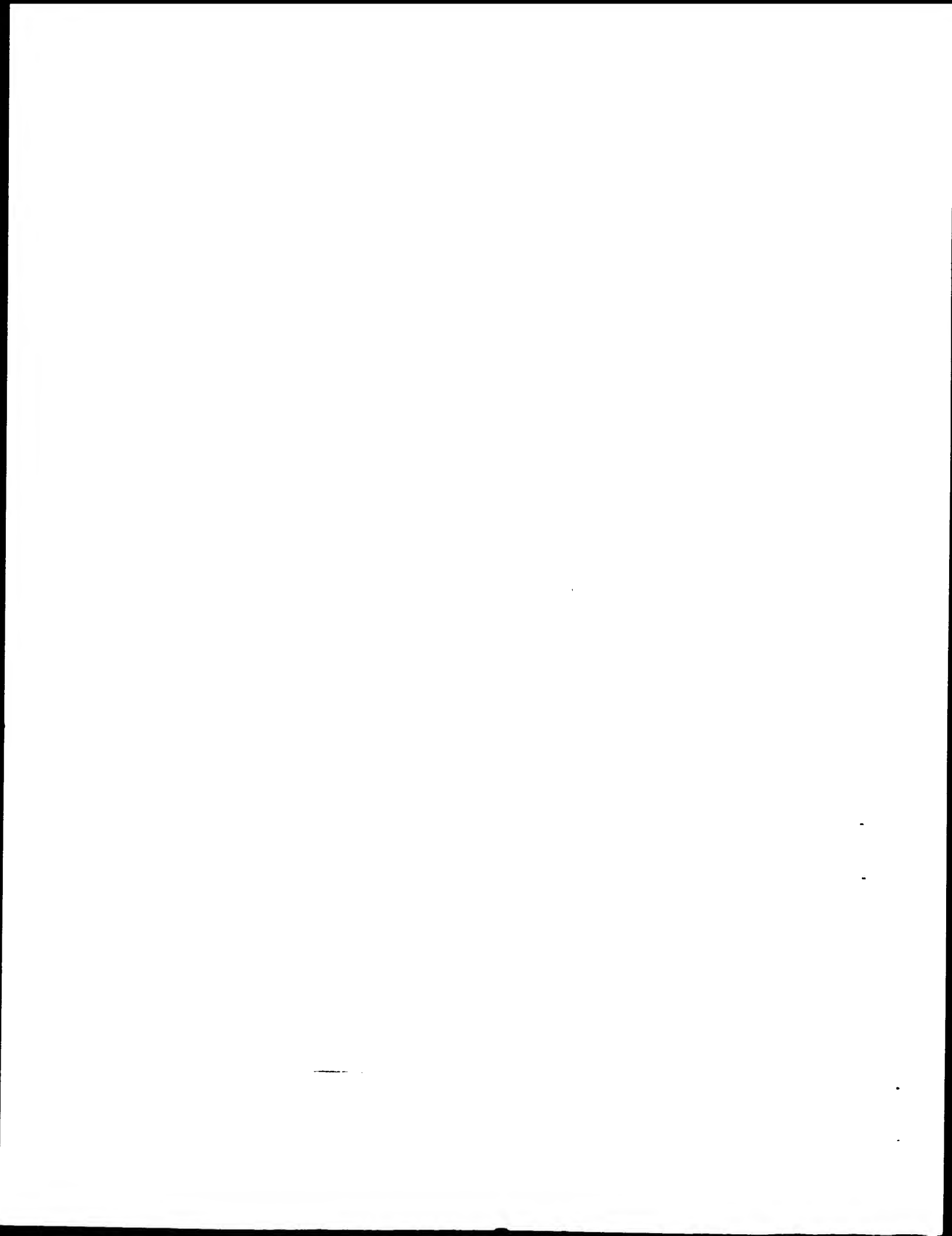
B7-2 antigen - human
N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48754; S39055
R:Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard
Science 262, 909-911, 1993
A:Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell pr
A:Reference number: A48754; MUID:94053735; PMID:7694363
A:Accession: A48754
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-329 <FRE>
A:Cross-references: GB:L25259; NID:g416368; PIDN:AAA58389.1; PID:g416369
A>Note: it is uncertain whether Met-1 or Met-7 is the initiator
R:Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza,
Nature 366, 76-79, 1993
A:Title: B70 antigen is a second ligand for CTLA-4 and CD28.
A:Reference number: S39055; MUID:94050123; PMID:7694153
A:Accession: S39055
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 7-329 <AZU>
A:Cross-references: GB:U04343; NID:g439838; PIDN:AAB03814.1; PID:g439839
C:Genetics:
A:Gene: GDB:CD86; CD28LG2
A:Cross-references: GDB:433597; OMIM:601020
A:Map position: 3q13.3-3q21
C:Superfamily: B7-2 antigen
C:Keywords: glycoprotein

Query Match 15.8%; Score 182; DB 1; Length 329;
Best Local Similarity 29.0%; Pred. No. 2.7e-07;
Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;

QY 18 EVATLSC---GHNVSVEELAQTRIVYQKEKKNVLTMM---SGDMNIWPEYKKNRTIFDI 69
DB 34 ETADLPQCFANSONQSLSLV---VFQDQENLVNEVLGKEKFDVSHSKYMGRTSFD- 89
QY 70 TNNLSIVILALRPSDEGTVECVLYKEDAFKREHLAEVTLVSVKADFTPTPSISDFEIPTS 129
DB 90 SDSWTLRLHNLQIKDKGLQYIIHKKPTGMIRIHMNSSELSVLANSFQPEI----VPIS 145
QY 130 NIR-----RIICSTSGGFPPEP-HLSWLENGEELNAINTV-----SQDPETELYAVS 175
DB 146 NITENVYINLTCSHIGYPEPKMSVL-----LRTKSTIEYDGMOKSDQNVTELYDVS 200
QY 176 SKLDF---NMTNHSFMCILIKYGLHVR 199
DB 201 ISLSVSFDPVTSNMTIFCILETDKTRL 227

RESULT 8
I49522
gene B7-2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I49522
R:Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Klu
J. Exp. Med. 178, 2185-2192, 1993
A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell
A:Reference number: I49522; MUID:94065585; PMID:7504059
A:Accession: I49522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:L25606; NID:g432478; PIDN:AAA79770.1; PID:g432479
C:Genetics:
A:Gene: B7-2
C:Superfamily: B7-2 antigen

Query Match 13.2%; Score 152; DB 2; Length 309;
Best Local Similarity 26.1%; Pred. No. 6.7e-05;



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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:20:25 ; Search time 13 Seconds
(without alignments)
689.145 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVIHVKVEKVA.....LRVNTQFNWNTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1149	100.0	288	1 CD80_HUMAN	P33681 homo sapien
2	738	64.2	299	1 CD80_RABIT	P42070 oryctolagus
3	561	48.8	306	1 CD80_MOUSE	Q00609 mus musculus
4	182	15.8	329	1 CD86_HUMAN	P42081 homo sapien
5	161	14.0	302	1 ICOL_HUMAN	O75144 homo sapien
6	152	13.2	309	1 CD86_MOUSE	P42082 mus musculus
7	150.5	13.1	322	1 ICOL_MOUSE	Q9JHJ8 mus musculus
8	140.5	12.2	330	1 CD86_RABIT	P42071 oryctolagus
9	134.5	11.7	583	1 C166_MOUSE	Q61490 mus musculus
10	133.5	11.6	583	1 C166_HUMAN	Q13740 homo sapien
11	129	11.2	221	1 BRFL_EBV	P03228 epstein-bar
12	127	11.1	526	1 BURY_HUMAN	Q13410 homo sapien
13	122.5	10.7	588	1 C166_CHICK	P42292 gallus gall
14	119	10.4	524	1 BURY_MOUSE	Q62556 mus musculus
15	116.5	10.1	1088	1 NCAL_XENLA	P16170 xenopus lae
16	115	10.0	761	1 NCA2_HUMAN	P13592 homo sapien
17	115	10.0	848	1 NCAL_HUMAN	P13591 homo sapien
18	110.5	9.6	321	1 TCE_FLIV	P11364 feline leuk
19	109.5	9.5	646	1 M018_HUMAN	P43121 homo sapien
20	109.5	9.5	853	1 NCAL_BOVIN	P31836 bos taurus
21	109	9.5	526	1 BURY_BOVIN	P18892 bos taurus
22	109	9.5	2029	1 LAR_DROME	P16621 drosophila
23	108.5	9.4	365	1 CXAR_MOUSE	P97792 mus musculus
24	107.5	9.4	333	1 AMAL_DROME	P15364 drosophila
25	106.5	9.3	858	1 NCAL_RAT	P13596 rattus norv
26	105	9.1	319	1 A33_HUMAN	Q99795 homo sapien
27	105	9.1	1091	1 NCAL_CHICK	P13590 gallus gall
28	104	9.1	1092	1 NCA2_XENLA	P36335 xenopus lae
29	103.5	9.0	725	1 NCA2_MOUSE	P13594 mus musculus
30	103.5	9.0	1115	1 NCAL_MOUSE	P13595 mus musculus
31	103	9.0	298	1 JAM2_HUMAN	P57087 homo sapien
32	102	8.9	1443	1 NEO1_CHICK	Q90610 gallus gall
33	101.5	8.8	403	1 RAGE_MOUSE	Q62151 mus musculus

ALIGNMENTS

RESULT 1

ID	CD80_HUMAN	STANDARD;	PRT;	288 AA.
AC	P33681:			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last annotation update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (CTLA-4 counter-receptor B7.1) (B7) (BBL).			
GN	CD80 OR CD28LG1 OR CD28LG OR LAB7.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymphoid;			
RX	MEDLINE=90010147; PubMed=2794510;			
RA	Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F., Nadler L.M.;			
RA	"B7, a new member of the Ig superfamily with unique expression on activated and neoplastic B cells."			
RT	J. Immunol. 143:2714-2722(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92307753; PubMed=1371173;			
RA	Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.;			
RT	"Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7."			
RL	Immunogenetics 36:175-181(1992).			
RN	[3]			
RP	SEQUENCE OF 35-38.			
RX	MEDLINE=91341422; PubMed=1714935;			
RA	Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J., White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;			
RT	"Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7."			
RL	J. Exp. Med. 174:625-631(1991).			
RN	[4]			
RP	CHARACTERIZATION.			
RX	MEDLINE=95088403; PubMed=7527824;			
RA	Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.;			
RT	"CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL."			
RL	J. Immunol. 154:97-105(1995).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.			
RX	MEDLINE=20125021; PubMed=10661405;			
RA	Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K., Jones E.Y., Stuart D.I., Davis S.J.;			
RT	"Structure and dimerization of a soluble form of B7-1."			
RL	Immunity 12:51-60(2000).			
CC	-I- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE			

P31398 manduca sex
P17948 h vascular
P78310 homo sapien
Q9qzs7 mus musculus
P04218 rattus norv
Q9xt56 bos taurus
P35969 mus musculus
P53767 rattus norv
P19320 homo sapien
Q9r044 rattus norv
P40199 homo sapien
P12960 mus musculus

QY 4 HFCGVIHTVEKEVATLSCGHNVSVVEELAQTRIVYQKEKKWLTMMSGDMNIWPEYKN 63
 Db 29 HFSGIGISQVTSKVEKMAALSDYNISDELARMRIYQKQDMYLSISGQVEVMPEYKN 88
 QY 64 RTIFDITNNLSIVTALRPSDEGYECVWLKYEDAKREHLAEVTLVKADFPPTPSISD 123
 Db 89 RTFFDITNNLSMLALRLSDKGYTCVQKNENGSPREHLTSVTLIRADFVPVPSITD 148
 QY 124 FEIPTSNIIRICSTGGFPPLHLSWLENGEELNAINTVSQDETELYAVSSKLDNFMT 183
 Db 149 IGHDPNPKVIRCSASGSGFPPLRLAWEDGELNAINTVSQDETELYAVSSKLDNFMT 208
 QY 184 TNHSPMCLIKYGLRVNQTFNNWTKOE 211
 Db 209 NNHSIVCLIKYGLSVSQIFPWSKPQE 236

RESULT 3
 CD80_MOUSE STANDARD: PRT; 306 AA.
 AC Q00609;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (B7).
 DE CD80 OR B7.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=91341422; PubMed=1714935;
 RA Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,
 RA White M., Fingerioth J.D., Gribben J.G., Nadler L.M.;
 RT "Structure, expression, and T cell costimulatory activity of the
 RT murine homologue of the human B lymphocyte activation antigen B7."
 RL J. Exp. Med. 174:625-631(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=93307789; PubMed=7686531;
 RA Selvakumar A., White P.C., Dupont B.;
 RT "Genomic organization of the mouse B-lymphocyte activation antigen
 RT B7."
 RL Immunogenetics 38:292-295(1993).
 CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
 CC INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
 CC MALIGNANCIES.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
 CC ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
 CC IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
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 CC -----
 CC EMBL; X60958; CAA43291.1; -.

DR EMBL; L12589; AAA37240.1; ALT SEQ.
 DR EMBL; L12585; AAA37240.1; JOINED.
 DR EMBL; L12586; AAA37240.1; JOINED.
 DR EMBL; L12587; AAA37240.1; JOINED.
 DR EMBL; L12588; AAA37240.1; JOINED.
 DR PIR; S17291; S17291.
 DR HSP; P33681; 1DR9.
 DR MGD; MGI:101775; Cg80.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00410; Ig_like; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 37
 FT CHAIN 38 306
 FT DOMAIN 38 246
 FT TRANSMEM 247 268
 FT DOMAIN 269 306
 FT DOMAIN 47 126
 FT DOMAIN 158 226
 FT DOMAIN 227 246
 FT DISULFID 54 119
 FT DISULFID 165 219
 FT CARBOHYD 93 93
 FT CARBOHYD 99 99
 FT CARBOHYD 149 149
 FT CARBOHYD 189 189
 FT CARBOHYD 210 210
 FT CARBOHYD 214 214
 SQ SEQUENCE 306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;

Query Match 48.8%; Score 561; DB 1; Length 306;
 Best Local Similarity 50.7%; Pred. No. 4.1e-40;
 Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY 12 VTKEVKEVATLSCGHNVSVVEELAQTRIVYQKEKKWLTMMSGDMNIWPEYKNRTIFDITN 71
 Db 42 LSKSKVDKVLPCRYNSPHEDESDRIYQKHDKVLSVIAGKLVKWPVEYKNRTLYDNT- 100
 QY 72 NLSIVILALRPSDEGYECVWLKYEDAKREHLAEVTLVKADFPPTPSISDEIFETSNI 131
 Db 101 TYSILILGLVLSDRGTYSYCVQKRGTYEVKHLALVLSIKADFTSPNTPSGNPSADT 160
 QY 132 RRIICSTGGFPPLHLSWLENGEELNAINTVSQDETELYAVSSKLDNFMTNHSFMCL 191
 Db 161 KRITCFASGGFPKPRFSLWLENGRELPGINTTISQDPESELYTSSQLDFTNTHIKCL 220
 QY 192 IKYGLRVNQTFNNWTKOEHPDN 216
 Db 221 IKYGAHVSEDFTWEKPPDP-PDS 244

RESULT 4
 CD86_HUMAN STANDARD: PRT; 329 AA.
 AC P42081; Q13655;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen) (CTLA-4 counter-receptor B7.2) (B70) (FUN-1) (BU63).
 GN CD86 OR CD28LG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94053735; PubMed=7694363;
 RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,

RA Restivo V.A. Jr., Lombard L.A., Gray G.S., Nadler L.M.;
 RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
 RL cell proliferation.";
 RN Science 262:909-911(1993).
 [2]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX MEDLINE=94050123; PubMed=7694153;
 RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
 RA Lanier L.L., Somoza C.;
 RT "B70 antigen is a second ligand for CTLA-4 and CD28.";
 RN Nature 366:76-79(1993).
 [3]
 RL SEQUENCE OF 7-329 FROM N.A.
 RP TISSUE=Foreskin;
 RX MEDLINE=95331831; PubMed=7541777;
 RA Jellis N.R., Wang S.S., Rennett P., Borriello F., Sharpe A.H.,
 RA Green N.R., Gray G.S.;
 RT "Genomic organization of the gene coding for the costimulatory human
 RT B-lymphocyte antigen B7-2 (CD86).";
 RL Immunogenetics 42:85-89(1995).
 [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95088403; PubMed=7527824;
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.;
 RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
 RL cell proliferation, cytokine production, and generation of CTL.";
 RN J. Immunol. 154:97-105(1995).
 [5]
 RP IDENTIFICATION AS CD86.
 RX MEDLINE=94348060; PubMed=7520767;
 RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
 RA Nadler L.M., Wakasa H., Tedder T.F.;
 RT "The B7-2 (B70) costimulatory molecule expressed by monocytes and
 RT activated B lymphocytes is the CD86 differentiation antigen.";
 RL Blood 84:1402-1407(1994).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
 CC MONOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD86 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L25259; AAA58389.1; -
 CC EMBL; U04343; AAB03814.1; -
 CC EMBL; U17722; AAA86473.1; -
 CC EMBL; U17717; AAA86473.1; JOINED.
 CC EMBL; U17718; AAA86473.1; JOINED.
 CC EMBL; U17719; AAA86473.1; JOINED.
 CC EMBL; U17721; AAA86473.1; JOINED.
 CC Genew; HGNC:1705; CD86.
 CC MIM; 601020; -
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003596; Ig_v.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PS00290; IG_MHC; FALSE_NEG.
 CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW

KW Receptor.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 329 T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
 FT DOMAIN 24 247 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 248 268 POTENTIAL.
 FT DOMAIN 269 329 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 150 225 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 40 110 POTENTIAL.
 FT DISULFID 157 218 POTENTIAL.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 27 27 K -> E (IN REF. 3).
 SQ SEQUENCE 329 AA; 37696 MW; 65D4F3826889CF7D CRC64;
 Query Match 15.8%; Score 182; DB 1; Length 329;
 Best Local Similarity 29.0%; Pred. No. 3.1e-08;
 Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;
 QY 18 EVATLSC---GHNVSVEELAQTRIIYQKQKKVLTMM---SGDMNIWPEYKKNRTIFDI 69
 DB 34 ETADLPQCFANSQNSLSLV---VFWDQENLVNLVEVLGKKEKFDVSHKVMGRTSFD- 89
 QY 70 TNNLSVILALRPSDEGTVCVLYKYEKADKREHLAEVTLVSKADFTTSPISDFEIPTS 129
 DB 90 SDSWTLRLHLQIKDKGLYQCIHHKPKTGMIRIHQMNSELSVLANFSQPEI---VPIS 145
 QY 130 NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTV-----SQDPETELYAVS 175
 DB 146 NITENVINLTSSIHGYPEPKKMSVL-----LRTKNSTIEYDGMQKSDQNMVTELYDVS 200
 QY 176 SKLDF---NMNTNHSFMCILKYGLRV 199
 DB 201 ISLSVSPDVTNMTIFCILETDKTRL 227
 RESULT 5
 ICOL_HUMAN STANDARD; PRT; 302 AA.
 ID ICOL_HUMAN STANDARD; PRT; 302 AA.
 AC O75144; Q9NRQ1; Q9HD18;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
 DE (B7-related protein-1) (B7RP-1).
 GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Dendritic cell;
 RX MEDLINE=20477846; PubMed=11023515;
 RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
 RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds
 RL ICOS.";
 RL Blood 96:2808-2813(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC TISSUE=Peripheral blood lymphocytes;
 RX MEDLINE=20465019; PubMed=11007762;
 RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
 RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
 RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
 RT "Characterization of a new human B7-related protein: B7RP-1 is the
 RT ligand to the co-stimulatory protein ICOS.";

RL Patent number WO0121796, 29-MAR-2001.
 CC -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
 CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
 CC TH2 PHENOTYPE.
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
 CC (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY
 CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND Peyer's
 CC PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
 CC CELLS. T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
 CC -!- DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOIESIS. IN THE YOLK
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
 CC 14.5 DPC.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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 CC
 DR EMBL; AF216747; AAF45149.1; -
 DR EMBL; AF199027; AAF34738.1; -
 DR EMBL; AX100591; CAC36463.1; -
 DR EMBL; AX100593; CAC36464.1; -
 DR EMBL; AF394451; AAK77544.1; -
 DR MGD; MGI:1354701; Icosl.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00410; Ig_Like; 1.
 DR B-cell activation; Immune response; Glycoprotein;
 KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 KW Alternative splicing.
 FT SIGNAL 1 46
 FT CHAIN 47 322
 FT DOMAIN 47 277
 FT TRANSMEM 278 298
 FT DOMAIN 299 322
 FT DOMAIN 55 145
 FT DOMAIN 178 250
 FT DOMAIN 31 38
 FT DOMAIN 289 292
 FT DISULFID 62 138
 FT DISULFID 185 243
 FT CARBOHYD 71 71
 FT CARBOHYD 120 120
 FT CARBOHYD 163 163
 FT CARBOHYD 200 200
 FT CARBOHYD 213 213
 FT CARBOHYD 252 252
 FT CARBOHYD 265 265
 FT VARSPLIC 321 322
 FT ISOFORM 2).

FT CONFLICT 237 237 R -> H (IN REF. 4 AND 5; CAC36464).
 SQ SEQUENCE 322 AA; 35960 MW; 55CCBA4AD12E47E6 CRC64;
 Query Match 13.1%; Score 150.5; DB 1; Length 322;
 Best Local Similarity 27.1%; Pred. No. 1.4e-05;
 Matches 65; Conservative 32; Mismatches 102; Indels 41; Gaps 12;
 QY 2 LGHFC--SGVHVTKVKVAVLSCGHNVSV-----ELAQRIYWKQKMKV-----L 48
 DB 38 LSLCAASAEETEVGAMVGSNVVLS-----IDPHRHFNLSGLYVYVWQENPEVSVYYL 92
 QY 49 TMMSSGDIMWPEYKKNRTIFDITN-----NLSIVILALRPDSDEGYECVWLKYKDAFKREH 104
 DB 93 PYKSPGINDVSSYKNGHLSLDSMKQGNFSYLNKNTVPDQTQETCRV--FMNTATELVK 150
 QY 105 LAE--VTLVSKADFPFP--SISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAIN 160
 DB 151 ILEEVYRLRVAANFSPVISTSDSNPQGE--RTYTCMSKNGYPEPNLYWT--NTDMSLID 208
 QY 161 TTVSQDP---ETELYAVSKLDFNMTNHSFMCILKYGHRLVN-----QTFFNNTTK 209
 DB 209 TALQNTVYLNKLGILDVISTLRLPWTSGRDVLCVENVALHQNITISISQAESFTGNNTK 268
 RESULT 8
 CD86_RABIT STANDARD; PRT; 330 AA.
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
 DE antigen).
 GN CD86.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHBB:HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules";
 RL Immunogenetics 42:217-220(1995).
 CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC
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 CC
 DR EMBL; D49842; BAA08642.1; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 22 POTENTIAL.


```
FT CHAIN 23 330 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.  
FT DOMAIN 23 247 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 248 268 POTENTIAL.  
FT DOMAIN 269 330 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.  
FT DOMAIN 150 225 IG-LIKE C2-TYPE DOMAIN.  
FT DISULFID 40 110 POTENTIAL.  
FT DISULFID 157 218 POTENTIAL.  
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 330 AA; 37142 MW; 935CDD65C57E3EE1 CRC64;  
  
Query Match 12.2%; Score 140.5; DB 1; Length 330;  
Best Local Similarity 27.4%; Pred. No. 9.7e-05;  
Matches 60; Conservative 34; Mismatches 84; Indels 41; Gaps 12;  
  
QY 18 EVATLSGCH-NVSYEELAAQRIYQKMKVLTWM-----SGDMNIWPEYKNTIFDITN- 71  
DB 34 KTADLPQFTNSQSRSELVVFWDQGRVLVYELFLGRKPDNDPKYIGRTSFDQESW 93  
  
QY 72 NLSVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADPPTPSISDFEPTSI 131  
DB 94 NLQHNVOIK--DKGVYCFVHHRGAKGLVPIYQMNSELSVLANTQPEIT---LISNI 147  
  
QY 132 RR-----IICSTSGGFPPLHSLWENGEELNAINTV-----SQDPETELY--AVSS 176  
DB 148 TRNSAINLTCSSVGQYPPKMKFF---VLKTENATTEYDGVIERSQDNVTGLYNISISG 203  
  
QY 177 KLDP-NMTTNSFMCILIKYGLHRLVNOTENWNTTQOEHP 214  
DB 204 SITFSDDIRNATYICVL-----QTESTETYSQ-HFP 233  
  
RESULT 9  
C166_MOUSE STANDARD; PRT: 583 AA.  
AC Q61490; 070136;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE C166 antigen precursor (Activated leukocyte-cell adhesion molecule)  
DE (ALCAM) (DM-GRASP protein).  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NFS;  
RX MEDLINE=97353242; PubMed=9209500;  
RA Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,  
RA Kobarg J., Starling G.C., Siadak A.W., Aruffo A.;  
RT "Characterization of mouse ALCAM (CD166): the CD6 binding domain is  
RT conserved in different homologs and mediates cross-species binding.";  
RL Eur. J. Immunol. 27:1469-1478(1997).  
RN [2]  
RN SEQUENCE OF 227-583 FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Brain;  
RX MEDLINE=94376084; PubMed=6089660;  
RA Kanki J.P., Chang S., Kuwada J.Y.;  
RT "The molecular cloning and characterization of potential chick  
RT DM-GRASP homologs in zebrafish and mouse.";  
RL J. Neurobiol. 25:831-845(1994).  
CC -1- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6, INVOLVED IN  
CC NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC  
CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
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CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF  
CC THE NERVOUS SYSTEM.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; U95030; AAC06342.1; -;  
DR EMBL; L25274; AAA37528.1; -;  
DR HSSP; Q13740; 1KJC.  
DR MGD; MGI:1313266; Alcam.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003600; Ig_Like.  
DR Pfam; PF00047; Ig; 5.  
DR SMART; SM00409; Ig; 3.  
DR SMART; SM00410; IG_Like; 2.  
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.  
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;  
KW Repeat; Signal.  
FT SIGNAL 1 27 POTENTIAL.  
FT CHAIN 28 583 CD166 ANTIGEN.  
FT DOMAIN 28 527 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 528 549 POTENTIAL.  
FT DOMAIN 550 583 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 36 120 IG-LIKE V-TYPE DOMAIN 1.  
FT DOMAIN 263 321 IG-LIKE C2-TYPE DOMAIN 1.  
FT DOMAIN 347 399 IG-LIKE C2-TYPE DOMAIN 2.  
FT DOMAIN 428 492 IG-LIKE C2-TYPE DOMAIN 3.  
FT DISULFID 43 113 POTENTIAL.  
FT DISULFID 157 220 POTENTIAL.  
FT DISULFID 270 313 POTENTIAL.  
FT DISULFID 354 392 POTENTIAL.  
FT DISULFID 435 485 POTENTIAL.  
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 227 232 PSQKT -> AAGIPA (IN REF. 2).  
FT CONFLICT 454 454 S -> F (IN REF. 2).  
SQ SEQUENCE 583 AA; 65161 MW; E7BAFA8FCA8F9489 CRC64;  
  
Query Match 11.7%; Score 134.5; DB 1; Length 583;  
Best Local Similarity 25.2%; Pred. No. 0.00063;  
Matches 38; Conservative 34; Mismatches 54; Indels 25; Gaps 7;  
  
QY 59 PEYKNTIFDITNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADPPT 118  
DB 84 PEYKDR--LSLSNLTUSIANAKISDEKRFVCMVLT-EDNVFEAPTLVKV-----PKQ 133  
  
QY 119 PSISDFE-----IPTSNIIRRI-ICSTSGGFPPLHSLWENGEELNAINTVS-----QD 166  
DB 134 PSKPEIVNKAPFLETDLQKLGDCISRDSYDGNITWYRNGKVLQPVGEVAILPKKEID 193  
  
QY 167 PETELXAVSKLDFNMTNH---SFMCLIKY 194  
DB 194 PGQLTVTSSLEYKTRTSRDIQMPFTCSVTY 224  
  
RESULT 10  
C166_HUMAN
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ID C166_HUMAN STANDARD; PRT; 583 AA.
AC Q13740; O60892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CD166 antigen precursor (Activated leukocyte-cell adhesion molecule) (ALCAM).
DE NCBI_TaxID=9606;
GN ALCAM OR MEMD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95279947; PubMed=7760007;
RA Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R., Francke U., Wang W.-C., Marquardt H., Neubauer M., Pesando J.M., Francke U., Haynes B.F., Aruffo A.;
RT "Cloning, mapping, and characterization of activated leukocyte-cell adhesion molecule (ALCAM), a CD6 ligand.";
RL J. Exp. Med. 181:2213-2220(1995).
RN [2]
RP SEQUENCE OF 2-583 FROM N.A.
RX MEDLINE=98161527; PubMed=9502422;
RA Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J., van Kooyk Y., Bloemers H.P., Swart G.W.;
RT "MEMD, a new cell adhesion molecule in metastasizing human melanoma cell lines, is identical to ALCAM (activated leukocyte cell adhesion molecule).";
RL Am. J. Pathol. 152:805-813(1998).
RN [3]
RP CD6-BINDING DOMAINS.
RX MEDLINE=96420463; PubMed=8823162;
RA Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.;
RT "Recognition of diverse proteins by members of the immunoglobulin superfamily: delineation of the receptor binding site in the human CD6 ligand ALCAM.";
RL Biochemistry 35:12287-12291(1996).
RN [4]
RP 3D-STRUCTURE MODELING OF 28-133.
RX MEDLINE=96060095; PubMed=8520490;
RA Bajorath J., Bowen M.A., Aruffo A.;
RT "Molecular model of the N-terminal receptor-binding domain of the human CD6 ligand ALCAM.";
RL Protein Sci. 4:1644-1647(1995).
CC -1- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF THE NERVOUS SYSTEM.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD166 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd166.htm".

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CC EMBL; L38608; RA059499.1; -;
CC EMBL; Y10183; CAA71256.1; -;
CC PDB; 1KJC; 03-APR-96.
CC Genew; HGNC:400; ALCAM.
CC MIM; 601662; -;
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003600; Ig_like.

DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Cell adhesion; immunoglobulin domain; glycoprotein; Transmembrane; Repeat; Signal; 3D-structure; Polymorphism.
FT SIGNAL 1 27
FT CHAIN 28 583
FT CD166 ANTIGEN.
FT DOMAIN 28 527
FT TRANSMEM 528 549
FT DOMAIN 550 583
FT DOMAIN 36 120
FT DOMAIN 150 227
FT DOMAIN 263 321
FT DOMAIN 347 399
FT DOMAIN 428 492
FT DISULFID 43 113
FT DISULFID 157 220
FT DISULFID 270 313
FT DISULFID 354 392
FT DISULFID 435 485
FT CARBOHYD 91 91
FT CARBOHYD 95 95
FT CARBOHYD 167 167
FT CARBOHYD 265 265
FT CARBOHYD 306 306
FT CARBOHYD 361 361
FT CARBOHYD 457 457
FT CARBOHYD 480 480
FT CARBOHYD 499 499
FT VARIANT 258 258
FT VARIANT 301 301
FT VARIANT M -> T.
FT /FTid=VAR_003907.
SQ SEQUENCE 583 AA; 65132 MW; E023FB3974A60284 CRC64;
Query Match 11.6%; Score 133.5; DB 1; Length 583;
Best Local Similarity 24.5%; Pred. No. 0.00076;
Matches 37; Conservative 35; Mismatches 54; Indels 25; Gaps 7;
QY 59 PEYKNRTIFDITNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADPPT 118
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 84 PEYKDR--LNLSENYTSLISNARISDEKRFVCMVLT--EDNVFEAPTIVKV-----FKQ 133
QY 119 PSISDFE-----IPTSNIIRI--ICSTSGGFPPEPHLSWLENGEELNAINTVT-----SQD 166
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 134 PSKEIVSKALFLTEQEQLKGLGDCISDSYDGNITWYRNGKVLHPLEGAVVILFKKEMD 193
QY 167 PETELYAVSSKLDNFMT---TNHSFMCLIKY 194
| | | | | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 194 PVTQLYTMSTLEVYKTKKADIQMPFTCSVTY 224
RESULT 11
BRFL_EBV
ID BRFL_EBV STANDARD; PRT; 221 AA.
AC P03228;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 33 kDa early protein (p33).
GN BARF1.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Sequin C., Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";


```

RL Nature 310:207-211(1984).
RN [2]
RP IDENTIFICATION OF PROTEIN.
RX MEDLINE=90059873; PubMed=2555151;
RA Wei M.X., Ooka T.;
RT "A transforming function of the BARF1 gene encoded by Epstein-Barr
RT virus.";
RL EMBO J. 8:2897-2903(1989).
CC -!- FUNCTION: BARF1 HAS TRANSFORMING ACTIVITY.
CC
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CC
CC EMBL: V01555; CA24809.1; -.
DR PIR: A03792; Q0BE48.
DR PIR: S33058; S33058.
DR InterPro: IPR003600; Ig_Like.
DR SMART: SM00410; IG_Like; 1.
KW Early protein; Oncogene.
SQ SEQUENCE 221 AA; 24471 MW; CA5A24D1EA28758E CRC64;

Query Match 11.2%; Score 129; DB 1; Length 221;
Best Local Similarity 27.0%; Pred. No. 0.00054;
Matches 43; Conservative 25; Mismatches 47; Indels 44; Gaps 8;

QY 18 EVATLSCGHNVSVVEELAQRIYVOK-----BKKMVLTMMSGDMNIWPE 60
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 19 QAVTAFLGFRVLTLS-----YWRYSLSGLPEIEVSWFKLGPGEQVLGRMHHDV-IFIE 71
QY 61 YKNRTIFDI---TNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEV---TLSV-- 112
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 72 WFERGFEDLHRSANTFLVVTAAINSHDGNLYCRMKLGTEVTKQEHLSVVKPLTSLVHS 131
QY 113 -KADFTPTSIDFPTSNIRRICTSGGFPPEHLSWL 150
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 132 ERSQEP-----DFSULT-----VTCTVNAFPHVQWL 159

RESULT 12
ID BUTY_HUMAN STANDARD; PRT; 526 AA.
AC Q13410;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Butyrophilin precursor (BT).
GN BTN1AL OR BTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=96201696; PubMed=8611614;
RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT "Cloning and sequence analysis of human Butyrophilin reveals a
RT potential receptor function.";
RL Biochim. Biophys. Acta 1306:1-4(1996).
CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.

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CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
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CC
CC EMBL: U39576; AAC50489.1; -.
DR Genew; HGNC:1135; BTN1AL.
DR MIM: 601610; -.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR003878; SPRY_domain.
DR InterPro: IPR003877; SPRY_receptor.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00449; SPRY; 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 26
FT CHAIN 27 526
FT DOMAIN 27 242
FT TRANSMEM 243 269
FT DOMAIN 270 526
FT CARBOHYD 55 55
FT CARBOHYD 215 215
SQ SEQUENCE 526 AA; 59004 MW; E9EACDF8DAF94D5 CRC64;

Query Match 11.1%; Score 127; DB 1; Length 526;
Best Local Similarity 27.5%; Pred. No. 0.0024;
Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps 10;

QY 16 VKEVATLSC--GHNVSVEELAQRIYVQKEKKMWLTMSG---DMNIWEYKNTTF--- 67
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 42 VGEAELPCLSPNASAEHL-ELRFRKVKVSPAVLVHRDGRGEQAEQMPYRGRATLVQD 100
QY 68 -DITNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVSKADFPPTSISDFEI 126
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 101 GIAGRVALRIGRVVSDGGEYTCF---FREDGSVEEL--VHLKVAALGSDPHIS-MQV 154
QY 127 PTSNIRRICTSGGFPPEHLSW-LENGELNAINITVSDPETE-LYAVSSKLDNFMT 184
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 155 QENGEICLECTSGVWPEPQVQWRTSKGKFP--STSESRNPDEGLFTVAASVIIRDTS 212
QY 185 NHPWCLIK 193
DB : | | |
DB 213 TKNVSCYIQ 221

RESULT 13
CL166_CHICK STANDARD; PRT; 588 AA.
ID CL166_CHICK
AC P42292;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CL166 antigen precursor (SCL glycoprotein) (BEN glycoprotein) (DM-
DE GRASP protein) (JC7 protein).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
RC TISSUE=Embryo;
RX MEDLINE=92030150; PubMed=1931049;
RA Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
RA McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;

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CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF
 CC PREGNANCY AND IS MAXIMAL DURING LACTATION.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U67065; AAB51034.1; -;
 CC EMBL; S80642; AAB35893.1; -;
 CC MGD; MG1:103118; Btndal.
 CC InterPro; IPR001870; Gamma_carboxylase.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003596; Ig_V.
 CC InterPro; IPR003878; SPRY domain.
 CC InterPro; IPR003877; SPRY_receptor.
 CC Pfam; PF00047; ig_1.
 CC Pfam; PF00622; SPRY; 1.
 CC SMART; SM00406; IGV; 1.
 CC SMART; SM00449; SPRY; 1.
 CC Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 CC SIGNAL 1 26
 CC CHAIN 27 524
 CC DOMAIN 27 247
 CC TRANSMEM 248 268
 CC TRANSMEM 269 524
 CC DOMAIN 56 56
 CC CARBOHYD 216 216
 CC CONFLICT 46 46
 CC CONFLICT 117 117
 CC CONFLICT 191 191
 CC CONFLICT 210 210
 CC CONFLICT 363 363
 CC CONFLICT 408 408
 CC CONFLICT 413 413
 CC CONFLICT 420 423
 CC CONFLICT 492 509
 CC
 CC QUERY MATCH 524 AA; 58406 MW; 333F4DE2C7704480 CRC64;
 CC
 CC Query Match 10.4%; Score 119; DB 1; Length 524;
 CC Best Local Similarity 23.8%; Pred. No. 0.011;
 CC Matches 44; Conservative 34; Mismatches 87; Indels 20; Gaps 7;
 CC
 CC QY 20 ATLSGCH--NVSVEELAQRIYWKKEKKVLTMMSGD-----MNIWPEYKNR-----TIFD 68
 CC Db 47 AELTCGSPNASSEYM---ELLWFRQTRSTAVLLYRDQEGQEQMTEYGRATLATAGL 103
 CC QY 69 ITNNLSIVILARPSDEGNYECVVLAKYKDAFKREHLAEVTLVKADFPPTSDFEPT 128
 CC Db 104 LGRATLLRDVRSQGGTYRC--LFRNDNDFEE---AAYLVKVAAGVDPQIS-MTVQE 157
 CC QY 129 SNIRRICSTSGFPFPHLSWLENGELNAINTVSDPETELVAVSSKLDENMTTNSHF 188
 CC Db 158 NGEMELECTSSGWYPEPQVQWRGTGNEMLPSTSESKKHNEGLFTVAVSMIARDSSIKNM 217
 CC QY 189 MCLIK 193
 CC Db 218 SCCIQ 222
 CC
 CC RESULT 15
 CC NCAL_XENLA
 CC ID NCAL_XENLA STANDARD; PRT; 1088 AA.
 CC AC P16170;
 CC DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
 DE 180).
 GN NCAM1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90098871; PubMed=2481269;
 RA Krieg P.A., Sakaguchi D.S., Kintner C.R.;
 RT "Primary structure and developmental expression of a large
 RT cytoplasmic domain form of Xenopus laevis neural cell adhesion
 RT molecule (NCAM).";
 RL Nucleic Acids Res. 17:10321-10335(1989).
 CC -!- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC NEURITES, ETC.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; N-CAM 180 (shown here) and
 CC N-CAM 140; are produced by alternative splicing.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURON AND IN PRESUMPTIVE NEURAL
 CC TISSUE.
 CC -!- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
 CC TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
 CC EARLY NEURAL DEVELOPMENT.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC
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 CC
 CC EMBL; M25696; AAA49909.1; -;
 CC PIR; S09600; IJXLNL.
 CC HSP; P56276; ITLK.
 CC InterPro; IPR003961; FN_III.
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003598; Ig_C2.
 CC Pfam; PF00041; fn3; 2.
 CC Pfam; PF00047; ig; 5.
 CC SMART; SM00060; FN3; 2.
 CC SMART; SM00408; IGC2; 5.
 CC Cell adhesion; Glycoprotein; Transmembrane; Repeat; Brain;
 CC Immunoglobulin domain; Alternative splicing; Signal.
 CC SIGNAL 1 19
 CC CHAIN 20 1088
 CC
 CC DOMAIN 20 705
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 706 723
 CC DOMAIN 724 1088
 CC CYTOPLASMIC (POTENTIAL).
 CC IG-LIKE C2-TYPE DOMAIN 1.
 CC IG-LIKE C2-TYPE DOMAIN 2.
 CC IG-LIKE C2-TYPE DOMAIN 3.
 CC IG-LIKE C2-TYPE DOMAIN 4.
 CC IG-LIKE C2-TYPE DOMAIN 5.
 CC FIBRONECTIN TYPE-III 1.
 CC FIBRONECTIN TYPE-III 2.
 CC HEPARIN-BINDING (POTENTIAL).
 CC PROBABLE.
 CC DISULFID 41 93
 CC DISULFID 136 186
 CC DISULFID 232 282
 CC DISULFID 323 379
 CC DISULFID 420 473

Search completed: January 6, 2003, 14:24:26
Job time : 15 secs

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OM protein - protein search, using sw model
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(without alignments)
1534.696 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCGVIHVKVEKVA.....LRVNTFNWNTTKQEHFDPN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organella:*
9: sp.phage:*
10: sp.plant:*
11: sp.priodont:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.rvirus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1118	97.3	288	6	O77684 macaca neme
2	1100	95.7	288	6	Q28499 macaca mula
3	1085	94.4	288	6	Q9BDN6 macaca mula
4	1085	94.4	289	6	Q28347 cercocobus
5	772	67.2	296	6	Q8WMZ2 sus scrofa
6	764	66.5	230	6	Q9N213 sus scrofa
7	762.5	66.4	288	6	Q9TT70 sus scrofa
8	762.5	66.4	297	6	Q9BE99 sus scrofa
9	761	66.2	229	6	Q9TT71 sus scrofa
10	743	64.7	292	6	Q9GMZ8 felis silve
11	743	64.7	292	6	O02758 felis silve
12	719	62.6	304	6	Q9TQX1 canis fami
13	717.5	62.4	236	6	O46405 bos taurus
14	705	61.4	235	6	Q9N0T0 canis fami
15	705	61.4	235	6	Q9TQ88 canis fami
16	603.5	52.5	321	11	O35187 rattus norv

17	602	52.4	290	11	Q62680	Q62680 rattus norv
18	601.5	52.3	321	11	Q62624	Q62624 rattus norv
19	596	51.9	321	11	O55202	Q55202 rattus norv
20	560	48.7	306	11	Q9R129	Q9R129 mus musculus
21	350	30.5	174	6	Q9GMZ9	Q9GMZ9 felis silve
22	349.5	30.4	173	6	Q95L17	Q95L17 felis silve
23	255.5	22.2	212	11	Q61332	Q61332 mus musculus
24	200.5	17.4	329	6	Q9XSX6	Q9XSX6 felis silve
25	200.5	17.4	332	6	Q9GMZ7	Q9GMZ7 felis silve
26	200.5	17.4	332	6	Q95L16	Q95L16 felis silve
27	188.5	16.4	280	6	Q9TTF1	Q9TTF1 canis fami
28	188.5	16.4	296	13	O42404	O42404 gallus gall
29	182	15.8	329	6	Q9TTF2	Q9TTF2 canis fami
30	178	15.5	323	6	Q9BDM2	Q9BDM2 cercopithe
31	177	15.4	323	6	Q9BDM9	Q9BDM9 macaca neme
32	177	15.4	323	6	Q9EDM4	Q9EDM4 macaca mula
33	176	15.3	275	6	Q9BDN9	Q9BDN9 papio anubi
34	176	15.3	323	6	Q9BDB8	Q9BDB8 cercocobus
35	171	14.9	284	6	Q9GL33	Q9GL33 bos taurus
36	162	14.1	313	11	O35531	O35531 rattus norv
37	161.5	14.1	325	6	O02838	O02838 sus scrofa
38	159	13.8	316	11	Q8VE98	Q8VE98 mus musculus
39	156.5	13.6	290	4	Q9NZQ7	Q9NZQ7 homo sapien
40	153	13.3	290	11	Q9EP73	Q9EP73 mus musculus
41	153	13.3	356	11	Q64381	Q64381 mus musculus
42	152	13.2	314	11	Q61238	Q61238 mus musculus
43	150	13.1	309	11	O91YV7	O91YV7 mus musculus
44	142	12.4	316	4	Q9BXR1	Q9BXR1 homo sapien
45	139.5	12.1	521	6	O46651	O46651 oryctolagus

ALIGNMENTS

RESULT 1

O77684 ID O77684 PRELIMINARY; PRT; 288 AA.
AC O77684;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE B7 protein.
DE B7.
GN Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kraus G., Hnatyszyn J.H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AR079519; AAC31555.1; -
DR HSSP; P33681; IDR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_Like; 1.
SQ SEQUENCE 288 AA; 33131 MW; 76BBC42839E9AB79 CRC64;

Query Match 97.3%; Score 1118; DB 6; Length 288;

Best Local Similarity 97.7%; Pred. No. 1.2e-91;

Matches 210; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LSHPFCGVIHVKVEKVAATLSCGHNVSVVELAQTRIVQKQKWLTMMSGDNINWPEY 61

Db 28 LSHPFCGVIHVKVEKVAATLSCGHNVSVVELAQTRIVQKQKWLTMMSGDNINWPEY 87

QY 62 KNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLTSVKADFPPTPSI 121

Db 88 KNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLTSVKADFPPTPSI 147

QY 122 SDFEIPSTNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDNF 181
 Db :|||||
 Db 148 TDFEIPSPNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGLHRLVNTQTFNNTTKQEHFPDN 216
 Db :|||||
 Db 208 MTNHSFMCILIKYGLHRLVNTQTFNNTPKQEHFPDN 242

RESULT 2

Q28499
 ID Q28499 PRELIMINARY; PRT; 288 AA.
 AC Q28499;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE B7 protein (CD80 protein precursor).
 GN B7 OR N939.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
 RX "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
 RT J. Immunol. 155:3946-3954(1995).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules.";
 RL Immunogenetics 0:0-0(2001).
 DR EMBL; U19840; AAA86706.1; -.
 DR EMBL; AF344849; AAK37609.1; -.
 DR HSSP; P33681; IDR9.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00410; IG_Like; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

Query Match 95.7%; Score 1100; DB 6; Length 288;
 Best Local Similarity 96.3%; Pred. No. 4.8e-90;
 Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGSGVIHVTKEVATLSCGHNVSVVEELAQTRIYQKWKVLTMMSGDMNIWPEY 61
 Db :|||||
 Db 28 LSHFCGSGVIHVTKEVATLSCGHNVSVVEELAQTRIYQKWKVLTMMSGDMNIWPEY 87
 QY 62 KNRTIFDTNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 121
 Db :|||||
 Db 88 KNRTIFDTNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 147
 QY 122 SDFEIPSTNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDNF 181
 Db :|||||
 Db 148 TDFEIPSPNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGLHRLVNTQTFNNTTKQEHFPDN 216
 Db :|||||
 Db 208 MTNHSFMCILIKYGLHRLVNTQTFNNTPKQEHFPDN 242

RESULT 3

Q9BDN6
 ID Q9BDN6 PRELIMINARY; PRT; 288 AA.
 AC Q9BDN6;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE CD80 protein.
 GN MNB71.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Cercopithecus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344839; AAK37535.1; -.
 DR HSSP; P33681; IDR9.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00410; IG_Like; 1.
 SQ SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 288;
 Best Local Similarity 95.3%; Pred. No. 1e-88;
 Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGSGVIHVTKEVATLSCGHNVSVVEELAQTRIYQKWKVLTMMSGDMNIWPEY 61
 Db :|||||
 Db 28 LSHFCGSGVIHVTKEVATLSCGHNVSVVEELAQTRIYQKWKVLTMMSGDMNIWPEY 87
 QY 62 KNRTIFDTNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 121
 Db :|||||
 Db 88 KNRTIFDTNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 147
 QY 122 SDFEIPSTNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDNF 181
 Db :|||||
 Db 148 TDFEIPSPNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGLHRLVNTQTFNNTTKQEHFPDN 216
 Db :|||||
 Db 208 MTNHSFMCILIKYGLHRLVNTQTFNNTPKQEHFPDN 242

RESULT 4

Q28347
 ID Q28347 PRELIMINARY; PRT; 289 AA.
 AC Q28347;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE B7 protein (fragment).
 GN B7.
 OS Cercopithecus torquatus (red-crowned mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Cercopithecus.
 OX NCBI_TaxID=9530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and


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RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
DR EMBL; U19833; AAA86700.1; -.
DR HSP; P33681; IDR9.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00410; Ig_like; 2.
FT NON_TER 289
SQ SEQUENCE 289 AA; 33030 MW; 5ED6A3F6A3C59297 CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 289;
Best Local Similarity 95.3%; Pred. No. 1e-88;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 LSHFCSGVIHVTKEVATLSCGHNVSEELAQTRIVYQKEKKMVLTMGDMNIWPEY 61
Db 28 LSHFCSGVIHVTKEVATLSCGHNVSEELAQTRIVYQKEKKMVLTMGDMNIWPEY 87
Qy 62 KNRTIFDITNLSIVILALRPSDECTYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 121
Db 88 KNRTIFDITNLSIVILALRPSDECTYECVVLKYEKDAFKREHLAEVTLVKADFPPTSI 147
Qy 122 SDFEIPTSNIRRIICSTSGGPPPEHLNENALNTVSDPETELYAVSSKLDNF 181
Db 148 TDFEIPPSNIRRIICSTSGGPPPEHLNENALNTVSDPETELYAVSSKLDNF 207
Qy 182 MTTNHSFVCLIKYGHRLVQTFNNTTKQEHFPDN 216
Db 208 MTTNHSFVCLIKYGHRLVQTFNNTTKQEHFPDN 242

RESULT 5
Q8WMZ2
ID Q8WMZ2 PRELIMINARY; PRT; 296 AA.
AC Q8WMZ2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE DB0.
GN DB0.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Tadaki D.K., Williams A., Lee K.P., Kirk A.D., Harlan D.M.;
RT direct human T-cell activation."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF45811; AAL58443.1; -.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
SQ SEQUENCE 296 AA; 33275 MW; 69E494237E679C98 CRC64;

Query Match 67.2%; Score 772; DB 6; Length 296;
Best Local Similarity 66.8%; Pred. No. 8.2e-61;
Matches 141; Conservative 28; Mismatches 42; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVIHVTKEVATLSCGHNVSEELAQTRIVYQKEKKMVLTMGDMNIWPE 60
Db 22 GLDFCISGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81
Qy 61 YKNTIFDITNLSIVILALRPSDECTYECVVLKYEKDAFKREHLAEVTLVKADFPPTPS 120
Db 82 YENRTFTDVTNNLCIVILALRPSDNGTVCVVQKRGERSYKLEHLTSVKLMVKADFPVPS 141
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLNENALNTVSDPETELYAVSSKLDNF 180
Db 142 ITALGNPSNIRRIICSTSGGPPPEHLNENALNTVSDPETELYAVSSKLDNF 201

Query Match 66.5%; Score 764; DB 6; Length 230;
Best Local Similarity 67.0%; Pred. No. 3.1e-60;
Matches 140; Conservative 26; Mismatches 43; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVIHVTKEVATLSCGHNVSEELAQTRIVYQKEKKMVLTMGDMNIWPE 60
Db 22 GLDFCISGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81
Qy 61 YKNTIFDITNLSIVILALRPSDECTYECVVLKYEKDAFKREHLAEVTLVKADFPPTPS 120
Db 82 YENRTFTDVTNNLCIVILALRPSDNGTVCVVQKRGERSYKLEHLTSVKLMVKADFPVPS 141
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLNENALNTVSDPETELYAVSSKLDNF 180
Db 142 ITALGNPSNIRRIICSTSGGPPPEHLNENALNTVSDPETELYAVSSKLDNF 201

RESULT 7
Q9TT70
ID Q9TT70 PRELIMINARY; PRT; 288 AA.
AC Q9TT70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE DB0.
GN DB0.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

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Qy 181 NMTNHSFVCLIKYGHRLVQTFNNTTKQEHFPDN 211
Db 202 NVTGNHSPVCLIKYGHRLVQTFNNTTKQEHFPDN 232

RESULT 6
Q9N2I3
ID Q9N2I3 PRELIMINARY; PRT; 230 AA.
AC Q9N2I3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE DB0.
GN DB0.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada M., Amai S., Hoshi M., Nio M., Ohi R.;
RT "Porcine CD80(B-7) mRNA, partial cds."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026121; BAA50700.2; -.
DR HSP; P33681; IDR9.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_like; 1.
KW Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 230 POTENTIAL.
SQ SEQUENCE 230 AA; 26028 MW; EB63AD172663C4A4 CRC64;

Query Match 66.5%; Score 764; DB 6; Length 230;
Best Local Similarity 67.0%; Pred. No. 3.1e-60;
Matches 140; Conservative 26; Mismatches 43; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVIHVTKEVATLSCGHNVSEELAQTRIVYQKEKKMVLTMGDMNIWPE 60
Db 22 GLDFCISGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81
Qy 61 YKNTIFDITNLSIVILALRPSDECTYECVVLKYEKDAFKREHLAEVTLVKADFPPTPS 120
Db 82 YENRTFTDVTNNLCIVILALRPSDNGTVCVVQKRGERSYKLEHLTSVKLMVKADFPVPS 141
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLNENALNTVSDPETELYAVSSKLDNF 180
Db 142 ITALGNPSNIRRIICSTSGGPPPEHLNENALNTVSDPETELYAVSSKLDNF 201

RESULT 7
Q9TT70
ID Q9TT70 PRELIMINARY; PRT; 288 AA.
AC Q9TT70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE DB0.
GN DB0.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

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RP  SEQUENCE FROM N.A.
RX  MEDLINE=20302785; PubMed=10843688;
RA  Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Wu D.,
RA  Fodor W.L., Mueller J.P., Mattis L.A., Rother R.P.;
RT  "Primary Structure and Functional Characterization of a Soluble,
RL  J. Immunol. 164:6340-6348(2000).
DR  EMBL; AF203443; AAF22750.1; -.
DR  HSP; P33681; 1DR9.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR003600; Ig_Like.
DR  InterPro; IPR003006; Ig_MHC.
DR  Pfam; PF00047; Ig; 2.
DR  SMART; SM00409; Ig; 1.
DR  SMART; SM00410; Ig_Like; 1.
KW  Signal.
FT  SIGNAL.
FT  CHAIN 1 29
FT  NON_TER 288
FT  CD80 PROTEIN.
SQ  SEQUENCE 288 AA; 32510 MW; 67E31D0FDB45D1C8 CRC64;

Query Match 66.4%; Score 762.5; DB 6; Length 288;
Best Local Similarity 66.5%; Pred. No. 5.5e-60;
Matches 141; Conservative 28; Mismatches 42; Indels 1; Gaps 1;

Qy 1 GLSHFCSGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPE 60
Db 22 GLFDGSGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81

Qy 61 YKRTIFDTNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADPPTPS 120
Db 82 YENRTFTDVTNNLCIVILALRLSDNGTYTCVVQKRGSGYKLEHLTSVKLMVKADFPVPS 141

Qy 121 ISDFEIPTSNIRRICTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 180
Db 142 ITALGNFSPNIRKIRCTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 201

Qy 181 NMTHNSFMCLIKYGHRLVNTQFNW-NTTKQE 211
Db 202 NVTGNHSEFMCLVKYGLTVSQTENWOKSAKRE 233

Qy 181 NMTHNSFMCLIKYGHRLVNTQFNW-NTTKQE 211
Db 202 NVTGNHSEFMCLVKYGLTVSQTENWOKSAKRE 233

RESULT 8
Q9BE99 PRELIMINARY; PRT; 297 AA.
AC Q9BE99;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 21, Last annotation update)
DE CD80 protein precursor.
GN CD80/B7-1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LANDRACE; TISSUE=ILEUM MUCOSA;
RA Wada M., Amae S., Sano N., Ishii T., Hoshi M., Sasaki H.,
RA Hayashi Y., Ohi R.;
RT "cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble
RT isoforms.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049760; BAB40952.1; -.
DR HSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_Like; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 29
FT POTENTIAL.
SQ SEQUENCE 1 29

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FT CHAIN 30 297 CD80 PROTEIN.
SQ SEQUENCE 297 AA; 33438 MW; 23109711EA63EF23 CRC64;

Query Match 66.4%; Score 762.5; DB 6; Length 297;
Best Local Similarity 66.5%; Pred. No. 5.8e-60;
Matches 141; Conservative 28; Mismatches 42; Indels 1; Gaps 1;

Qy 1 GLSHFCSGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPE 60
Db 22 GLFDGSGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81

Qy 61 YKRTIFDTNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADPPTPS 120
Db 82 YENRTFTDVTNNLCIVILALRLSDNGTYTCVVQKRGSGYKLEHLTSVKLMVKADFPVPS 141

Qy 121 ISDFEIPTSNIRRICTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 180
Db 142 ITALGNFSPNIRKIRCTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 201

Qy 181 NMTHNSFMCLIKYGHRLVNTQFNW-NTTKQE 211
Db 202 NVTGNHSEFMCLVKYGLTVSQTENWOKSAKRE 233

Qy 181 NMTHNSFMCLIKYGHRLVNTQFNW-NTTKQE 211
Db 202 NVTGNHSEFMCLVKYGLTVSQTENWOKSAKRE 233

RESULT 9
Q9TT71 PRELIMINARY; PRT; 229 AA.
ID Q9TT71
AC Q9TT71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CD80 protein precursor.
GN CD80 OR CD80/B7-1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Wada M., Amae S., Hoshi M., Nio M., Ishii T., Sano N., Sasaki H.,
RA Ohi R.;
RT "Splicing Isoform of Porcine CD80.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF203442; AAF22749.1; -.
DR EMBL; AB038153; BAA90764.1; -.
DR HSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_Like; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 29
FT CD80 PROTEIN.
SQ SEQUENCE 229 AA; 25900 MW; C3AD172663C4A4ED CRC64;

Query Match 66.2%; Score 761; DB 6; Length 229;
Best Local Similarity 67.8%; Pred. No. 5.6e-60;
Matches 139; Conservative 26; Mismatches 40; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPE 60
Db 22 GLFDGSGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81

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FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 304 B7-1 PROTEIN.
SQ SEQUENCE 304 AA; 34454 MW; 09E082F6BB06C94F CRC64;

Query Match 62.6%; Score 719; DB 6; Length 304;
Best Local Similarity 60.5%; Pred. No. 4.4e-56;
Matches 130; Conservative 36; Mismatches 49; Indels 0; Gaps 0;

QY 2 LSHFCSGVHVTKEVATLSCGHNVSVEELAQTRIYWKQEKKMLVLTMMSGDMNIWPEY 61
DB 28 LFYFCSGIIQVNTKVKAVLSCDYNISTELMKVRIYWKQDEVLAVTSGQTKVWSKY 87
QY 62 KNRFTIDTNLNSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVSKADFPVPSI 121
DB 88 ENRTFADFTNLSIVIMALRLSDNGKTYCIQVTEKRSYKVKHMTSVMLLVRADEFVPSI 147
QY 122 SDFEIPTSNIRRIICSTSGGFPPEHLVSWLENGEELNAINTVSQDPETELYAVSSKLDNF 191
DB 148 TDLGNPSHDIKRMCTSGGFPKPHLSWNEEELNAINTVSQDPDTELYTISSELDNF 207
QY 182 MTTNHSFMCILIKYGLRVNQTNNWTTKOEHPDN 216
DB 208 ITSNSHFVCLVKYGLDITVSIQIFNWKQSVPEHPNN 242

RESULT 13
ID O46405 PRELIMINARY; PRT; 296 AA.
AC O46405;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CD80 anitgen precursor (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99115507; PubMed=9914337;
RA Parsons K.R., Howard C.;
RT "Cloning of cattle CD80."
RL Immunogenetics 49:231-234(1999).
DR EMBL; Y09950; CAA71081.1; .
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_Like; 1.
KW SIGNAL.
FT SIGNAL 1 25 POTENTIAL.
FT NON_TER 296 296
SQ SEQUENCE 296 AA; 33618 MW; 7ADB11FB5F532EF5 CRC64;

Query Match 62.4%; Score 717.5; DB 6; Length 296;
Best Local Similarity 63.2%; Pred. No. 5.8e-56;
Matches 134; Conservative 28; Mismatches 47; Indels 3; Gaps 2;

QY 1 GLSHFCSGVI--HVTKEVATLSCGHNVSVEELAQTRIYWKQEKKMLVLTMMSGDMNIW 58
DB 27 GLFYFCSGITPKSVTKRKVETVMSLSDYNTSTELSLRIYWKQDKSMVLAAILPGKVQVW 86
QY 59 PEYKNTFTIDTNLNSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADFP 117
DB 87 PEYKNTFTIDTNLNSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADFP 146
QY 118 TPSISDFEIPTSNIRRIICSTSGGFPPEHLVSWLENGEELNAINTVSQDPETELYAVSSK 177
DB 147 VPTINDLGNPSNIRRIICSTSGGFPPEHLVSWLENGEELNAINTVSQDPETELYAVSSK 206

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QY 178 LDFNMTNHSFMCILIKYGLRVNQTNNWTTK 209
DB 207 LDFNMTNHSFMCILIKYGLRVNQTNNWTTK 238

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RESULT 14

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ID Q9N0T0 PRELIMINARY; PRT; 235 AA.
AC Q9N0T0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE T-cell co-stimulatory protein B7-1.
GN B7-1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Khatlani T., Ma Z., Onishi T.;
RT "Cloning and Sequencing of canine cDNA encoding T-cell co stimulatory molecule B7-1."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257653; AAF69006.1; -.
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_Like; 1.
SQ SEQUENCE 235 AA; 26933 MW; C0EA51DA9FB224E3 CRC64;

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Query Match 61.4%; Score 705; DB 6; Length 235;

Best Local Similarity 61.5%; Pred. No. 5.7e-55;

Matches 128; Conservative 33; Mismatches 47; Indels 0; Gaps 0;

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QY 2 LSHFCSGVHVTKEVATLSCGHNVSVEELAQTRIYWKQEKKMLVLTMMSGDMNIWPEY 61
DB 28 LFYFCSGIIQVNTKVKAVLSCDYNISTELMKVRIYWKQDEVLAVTSGQTKVWSKY 87
QY 62 KNRFTIDTNLNSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVSKADFPVPSI 121
DB 88 ENRTFADFTNLSIVIMALRLSDNGKTYCIQVTEKRSYKVKHMTSVMLLVRADEFVPSI 147
QY 122 SDFEIPTSNIRRIICSTSGGFPPEHLVSWLENGEELNAINTVSQDPETELYAVSSKLDNF 181
DB 148 TDLGNPSHDIKRMCTSGGFPKPHLSWNEEELNAINTVSQDPDTELYTISSELDNF 207
QY 182 MTTNHSFMCILIKYGLRVNQTNNWTTK 209
DB 208 ITSNSHFVCLVKYGLDITVSIQIFNWKQCK 235

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RESULT 15

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ID Q9TQ58 PRELIMINARY; PRT; 235 AA.
AC Q9TQ58;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Secreted B7-1 protein precursor.
GN CD80.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7

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